

SEQUENCE LISTING

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MUNSTER, MATTHEW
ALLAN, DEBORAH

<120> METHODS TO IDENTIFY SIGNAL SEQUENCES

<130> UTSD:772US

<140> UNKNOWN

<141> 2001-10-31

<150> 60/300,309

<151> 2001-06-21

<160> 324

<170> PatentIn Ver. 2.1

<210> 1

<211> 884

<212> DNA

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<222> (608)..(884)

<223> N = A, C, G or T/U

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<213> Homo sapiens

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 <222> (1)..(92)
 <223> XAA = ANYTHING

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			20					25					30		
Gly	Xaa	Lys	Tyr	His	Xaa	Cys	Ser	Gly	Phe	Xaa	Xaa	Leu	Xaa	Xaa	Gly
			35				40					45			
Leu	Xaa	Arg	Glu	Xaa	Leu	Ser	Leu	Pro	Leu	Thr	Lys	Gly	Ser	Asp	Ser
	50					55					60				
Thr	Leu	Xaa	Pro	Arg	Ala	Ser	Ser	Ser	Lys	Lys	Leu	Asn	Asn	Asn	Asn
65					70					75					80
Ser	Ser	Phe	Tyr	Thr	Gly	Val	Tyr	Ile	Leu	Ile	Xaa	Ala	Gly	Ala	Leu
				85					90					95	
Met	Met	Leu	Val	Gly	Phe	Leu	Gly	Cys	Cys	Gly	Ala	Val	Gln	Glu	Ser
			100					105					110		
Gln	Cys	Met	Leu	Gly	Leu	Phe	Phe	Gly	Leu	Pro	Leu	Gly	Asp	Ile	Arg
		115					120					125			
His	Asn	Ser	Cys	Gly	His	Leu	Gly	Ile	Phe	Pro	Gln	Gly	Gly	Asp	Gly
	130					135					140				
Ser	Pro	Gly	Val	Leu	Gln	Gly	His	Leu	Gln	Gln	Ala	Glu	Asn	Gln	Gly
145				150					155					160	
Ala	Pro	Ala	Gly	Asn	Ala	Glu	Ser	His	Pro	Leu	Cys	Val	Glu	Leu	Leu
			165						170					175	
Trp	Phe	Gly	Trp	Gly	Arg	Gly	Thr	Val	Tyr	Leu	Arg	His	Leu	Pro	Gln
			180					185					190		
Glu	Gly	Arg	Thr	Arg	Asn	Leu	His	Arg	Glu	Val	Leu	Ser	Cys	His	Gln
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Arg	Gly	Leu	Arg	Gln	Ile	Pro	His	His	Arg	Arg	Ser	Gly	His	Arg	His
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Cys	Arg	Gly	His	Asp	Ile	Trp	His	Asp	Leu	Gln	Tyr	Asp	Leu	Val	Leu
225				230					235					240	
Cys	Tyr	Pro	Gln	Glu	Pro	Arg	Asp	Gly	Leu	Glu	Ser	Ala	Tyr	Ile	Pro
			245					250					255		
Glu	Gln	Glu	Ser	Leu	Pro	Met	Lys	Ile	Gly	Gly	Ile	Phe	Cys	Leu	Phe

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265

270

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 275 280 285

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<212> DNA

<213> Homo sapiens

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 tgaaagcagt gggaaggatg ctgggggttg cagcaatata aaactccagg gcagggccca 240
 ggccaactcc tgtaaggaat gcaaattccag caagaagtcc cagtcttttc tgttcagttt 300
 catggctatg aggtgttgcc atcagccaaa tcatcaatat cagggagccc aaggcagaca 360
 gcagggccagc ctgaatgaaa tgagtgacca tatggacata ggcccctgca gccgccacaa 420
 acatacaaag ggcaaaactt gcatagacct tcttcaggtg ctgctgcggt gacgggggta 480
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<211> 162

<212> PRT

<213> Homo sapiens

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Ile Thr Pro Ser Thr Gln Gln His Leu Lys Lys Val Tyr Ala Ser Phe
 20 25 30

Ala Leu Cys Met Phe Val Ala Ala Ala Gly Ala Tyr Val His Met Val
 35 40 45

Thr His Phe Ile Gln Ala Gly Leu Leu Ser Ala Leu Gly Ser Leu Ile
 50 55 60

Leu Met Ile Trp Leu Met Ala Thr Pro His Ser His Glu Thr Glu Gln
 65 70 75 80

Lys Arg Leu Gly Leu Leu Ala Gly Phe Ala Phe Leu Thr Gly Val Gly
 85 90 95

Leu Gly Pro Ala Leu Glu Phe Cys Ile Ala Val Asn Pro Ser Ile Leu
 100 105 110

Pro Thr Ala Phe Met Gly Thr Ala Met Ile Phe Thr Cys Phe Thr Leu
 115 120 125

Ser Ala Leu Tyr Ala Arg Arg Arg Ser Tyr Leu Phe Leu Gly Gly Ile
 130 135 140

Leu Met Ser Ala Leu Ser Leu Leu Leu Leu Ser Ser Leu Gly Asn Val
 145 150 155 160

Phe Phe

<210> 5
 <211> 454
 <212> DNA
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 gtacatacac aaaaaagtta ctggaatgct cggaataaga ttgtttttct gttgtcattt 180
 ttgctttttt tacaagggtt tttttctcct ttgagattat aatgaacatg gtcacaccac 240
 aagtaaagtc agaagtagga cagagaacgc tccgaaggct gggtttggtca tccgagatca 300
 ttaaaaatgg ctgaccctaa caatatgtac aaaaatataa aatgtaaata aaaaatacaa 360
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 tttttcctcc cctggtcgac gcggccgcga attc 454

<210> 6
 <211> 144
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Tyr Phe Leu Phe Thr Phe Tyr Ile Phe Val His Ile Val Arg Val Ser
 35 40 45
 His Phe Ser Arg Met Thr Lys Pro Ala Phe Gly Ala Phe Ser Val Leu
 50 55 60
 Leu Leu Thr Leu Leu Val Val Pro Cys Ser Leu Ser Gln Arg Arg Lys
 65 70 75 80
 Lys Thr Leu Lys Lys Gln Lys Gln Gln Lys Asn Asn Leu Ile Pro Ser
 85 90 95
 Ile Pro Val Thr Phe Leu Cys Met Tyr Leu Ala Val Leu Val Val Gly
 100 105 110
 Leu Tyr Glu Met Val Lys Lys Ala Lys Asp Lys Arg Phe Leu Phe Phe

115

120

125

Ser Phe Phe Val Tyr Glu Val Ala Val Tyr Phe Phe Trp Pro Gly Ser
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<210> 7

<211> 478

<212> DNA

<213> Homo sapiens

<400> 7

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catgtatgtg acttagatac tgctttttgg gaggttaaga gtagcatgaa gaacttaaga 180
tgacgataag agtctaaatt tttagtttca aggtttcaat agaatgtgga tatattcaaa 240
actttcaaaa aggacagtgt ttagaaaggg taaaactagg acacagaaaa cactgggaat 300
taccacgacc cccaagtgtc tccggctcca ggaaataacc attcatgtgt ttgctggagg 360
tcacacaatt ttcccttatt acctggtgca aaatgactca tcacttccca aaagcttctt 420
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<210> 8

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<212> PRT

<213> Homo sapiens

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Phe Glu Lys Lys Leu Leu Gly Ser Asp Glu Ser Phe Cys Thr Arg Gly
 20 25 30

Lys Ile Val Pro Pro Ala Asn Thr Met Val Ile Ser Trp Ser Arg Lys
 35 40 45

His Leu Gly Val Val Val Ile Pro Ser Val Phe Cys Val Leu Val Leu
 50 55 60

Pro Phe Leu Asn Thr Val Leu Phe Glu Ser Phe Glu Tyr Ile His Ile
 65 70 75 80

Leu Leu Lys Pro Asn Lys Phe Arg Leu Leu Ser Ser Ser Val Leu His
 85 90 95

Ala Thr Leu Asn Leu Pro Lys Ser Ser Ile Val Thr Tyr Met Met Ser
 100 105 110

Trp Ala Phe Ser Glu Pro Trp Arg Thr Leu Lys Gly Arg Ile Ala Ala
 115 120 125

Phe Leu Lys Gln Ile Gly Phe Leu Met Ser Phe Gly Ser Pro Cys Leu
 130 135 140

Leu Leu Met Leu Gly Ser
 145 150

<210> 9
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 <223> N = A, C, G or T/U

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 agtaactcca gtcacttccc ctgccacgtc ccaggctgcct agggaggcag tcagggttcac 180
 ctggtatacc tcttgaccag aagctgcctg aaggctcagc cctggcacca agatgctcct 240
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 gagcagctgg tcagctgggg actggctcct cgacagaaag gcctggaact cctgctctct 360
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 aagaagtacc cggangcccg ggcgcctgnc cggtgctcg cgtacaggan cccancgag 660
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 Gly Xaa Leu Gly Leu Xaa Gly Xaa Pro Val Arg Glu His Pro Xaa Arg
 35 40 45
 Arg Pro Gly Xaa Arg Val Leu Leu Ala Pro Trp Ala Pro Pro Gln Ser
 50 55 60

Pro Arg Arg Pro Glu Leu Pro Asp Leu Ala Xaa Glu Pro Arg Ala His
 65 70 75 80
 Ile Pro Val Arg Ile Lys Glu Gln Val Val Gly Leu Leu Ala Trp Asn
 85 90 95
 Asn Cys Ser Cys Glu Ser Ser Gly Gly Gly Leu Pro Leu Pro Phe Gln
 100 105 110
 Lys Gln Val Arg Ala Ile Asp Leu Thr Lys Ala Phe Asp Pro Ala Glu
 115 120 125
 Leu Arg Ala Ala Ser Ala Thr Arg Glu Gln Glu Phe Gln Ala Phe Leu
 130 135 140
 Ser Arg Ser Gln Ser Pro Ala Asp Gln Leu Leu Ile Ala Pro Ala Asn
 145 150 155 160
 Ser Pro Leu Gln Tyr Pro Leu Gln Gly Val Glu Val Gln Pro Leu Arg
 165 170 175
 Ser Ile Leu Val Pro Gly Leu Ser Leu Gln Ala Ala Ser Gly Gln Glu
 180 185 190
 Val Tyr Gln Val Asn Leu Thr Ala Ser Leu Gly Thr Trp Asp Val Ala
 195 200 205
 Gly Glu Val Thr Gly Val Thr Leu Thr Gly Glu Gly Gln Ala Asp Leu
 210 215 220
 Thr Leu Val Ser Pro Gly Leu Asp Gln Leu Asn Arg Gln Leu Gln Leu
 225 230 235 240
 Val Thr Tyr Ser Ser Arg Ser Tyr Gln Thr Asn Thr Ala Gly Ser
 245 250 255

<210> 11
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 <212> DNA
 <213> Homo sapiens

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<210> 12

<211> 159
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 <213> Homo sapiens

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Gly	Gly	Asp	Glu	Lys	Met	Val	Leu	Leu	Thr	Ala	Val	Leu	Leu	Leu	Leu
			20					25					30		
Ala	Ala	Tyr	Ala	Gly	Pro	Ala	Gln	Ser	Leu	Gly	Ser	Phe	Val	His	Cys
			35				40					45			
Glu	Pro	Cys	Asp	Glu	Lys	Ala	Leu	Ser	Met	Cys	Pro	Pro	Ser	Pro	Leu
	50					55					60				
Gly	Cys	Glu	Leu	Val	Lys	Glu	Pro	Gly	Cys	Gly	Cys	Cys	Met	Thr	Cys
65					70					75					80
Ala	Leu	Ala	Glu	Gly	Gln	Ser	Cys	Gly	Val	Tyr	Thr	Glu	Arg	Cys	Ala
				85					90					95	
Gln	Gly	Leu	Arg	Cys	Leu	Pro	Arg	Gln	Asp	Glu	Glu	Lys	Pro	Leu	His
			100					105					110		
Ala	Leu	Leu	His	Gly	Arg	Gly	Val	Cys	Leu	Asn	Glu	Lys	Ser	Tyr	Arg
			115				120						125		
Glu	Gln	Val	Lys	Ile	Glu	Arg	Asp	Ser	Arg	Glu	His	Glu	Glu	Pro	Thr
	130					135					140				
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145					150					155					

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<222> (527)..(938)

<223> N = A, C, G or T/U

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tcattttttca	tgcacaacct	ttccccagc	gcaaaagact	gttactttat	tattgtattc	180
aaaatttcatt	gtgtatatta	ctacaaagac	aaccccaaac	caattttttt	cctgcgaagt	240
ttaatgatcc	acaagtgtat	atatgaaatt	ctcctccttc	cttgccccc	tctctttctt	300
ccctctttcc	cctccagaca	ttctagtttg	tggagggtta	tttaaaaaaa	caaaaaagga	360
agatgggtcaa	gtttgtaaaa	tatttgtttg	tgctttttcc	ccctccttac	ctgaccccct	420
acgagttttac	aggtctgtgg	caatactctt	aaccataaga	attgaaatgg	tgaagaaca	480

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gatagcagat gtcttttaaat gaaatacatg tatattgngt atggacttaa ttatgcacat 660
gctcagatgt gtagacatcc tncgnatatt tacataacat atngaggtaa tagatagggg 720
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<213> Homo sapiens

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<220>
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<223> XAA = ANYTHING

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      20             25             30

Gly Pro Phe Pro Xaa Gly Ile Phe Pro Arg Xaa Xaa Leu Gly Val Lys
      35             40             45

Lys Ala Gln Arg Val Trp Gly Pro Xaa Asn Leu Arg Ser Lys Gln Xaa
      50             55             60

Leu Glu Asn Xaa Ser Arg Tyr Ile Pro Leu Ser Ile Thr Ser Ile Cys
      65             70             75             80

Tyr Val Asn Xaa Arg Arg Met Ser Thr His Leu Ser Met Cys Ile Ile
      85             90             95

Lys Ser Ile Xaa Asn Ile His Val Phe His Leu Lys Thr Ser Ala Ile
      100            105            110

Cys Met Tyr Gln Lys Cys Lys Leu Arg Ser Lys Trp Leu Cys Leu Ser
      115            120            125

Val Tyr Val Leu Leu Tyr Xaa Ser Ser Ile Val Phe Gln Tyr Phe Glu
      130            135            140

Pro Leu Val Tyr Thr Cys Phe Phe Thr Ile Ser Ile Leu Met Val Lys
      145            150            155            160

Ser Ile Ala Thr Asp Leu Thr Arg Arg Gly Ser Gly Lys Glu Gly Glu
      165            170            175

Lys Ala Gln Thr Asn Ile Leu Gln Thr Pro Ser Ser Phe Phe Val Phe

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180	185	190
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195	200	205
Lys Glu Arg Gly Ala Arg Lys Glu Glu Asn Phe Ile Tyr Thr Leu Val		
210	215	220
Asp His Thr Ser Gln Glu Lys Asn Trp Phe Gly Val Val Phe Val Val		
225	230	235 240
Ile Tyr Thr Met Asn Phe Glu Tyr Asn Asn Lys Val Thr Val Phe Cys		
245	250	255
Thr Gly Gly Lys Val Val His Glu Lys Asn Lys Asn Ser Cys Trp Asp		
260	265	270
Phe Ile Met Leu Leu Thr Val Trp Phe Val Trp Phe Cys Leu Leu Leu		
275	280	285
Ile Phe Ser Leu Leu Leu Pro Ala Trp Leu Cys Gln Thr Asn Gln Gly		
290	295	300
Ser		
305		

<210> 15
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 <212> DNA
 <213> Homo sapiens

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 gttcctgctc agtttttggtc ttttttggtg cattggtctc ctcaactttca ctctctgaga 180
 tctcctcaact ccgaccctgc ttgttgacct ttgggggtgga ggcttctctc actcgggcct 240
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 ttccccacag ctgtggtctg ggaagcagga tctccaagtt tccagtgtgg gcacctggaa 540
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 <212> PRT
 <213> Homo sapiens

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Pro Ala Val Pro Ser Tyr Gln Gln Phe Gln Val Pro Thr Leu Glu Thr
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 Trp Arg Ser Cys Phe Pro Asp His Ser Cys Gly Glu Leu Gly Val Glu
 35 40 45
 Gln Arg Ser Phe Cys Ile Gln Leu Pro Arg Gln Arg Arg Met Gly Ser
 50 55 60
 Pro Gln Pro Glu Glu Arg His Asp Arg Ile Lys Thr Arg Cys Gln Gly
 65 70 75 80
 Val Asp Gly Arg Lys Arg Pro Leu Gly Pro Gly Lys Asn Asp Arg Gly
 85 90 95
 Ala Gly Pro Pro Leu Glu Gly Ser Ala Arg Pro Ala Val Met Ala Lys
 100 105 110
 Leu Arg Ser Pro Gly Arg Gln Pro Arg Arg Pro Glu Arg Lys Pro Pro
 115 120 125
 Pro Gln Arg Ser Thr Ser Arg Val Gly Val Arg Arg Ser Gln Arg Val
 130 135 140
 Lys Val Arg Arg Pro Met His Gln Lys Arg Pro Lys Leu Ser Arg Asn
 145 150 155 160
 Ser Leu Gly His Ser Leu Pro Pro Ile Trp Ile Ala Trp Thr Gly Gly
 165 170 175
 Ala Leu Met Met Met Ala Ala Ala Thr Leu Gly Ile Ser Thr Arg Thr
 180 185 190
 Thr Glu Ala Arg Pro Pro Gly Ser
 195 200

<210> 17
 <211> 284
 <212> DNA
 <213> Homo sapiens

<400> 17
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 tgtattccag aactcggcga tgtaccaggt cacggagtag ttctcctcgc accagtccag 180
 cgtggagggtc gtggggcccc agtagccctc tcggtccgcg gccggagcca tcacgccgcc 240
 gccgccgcgcg cccaggcgct ccgcgtcgac gcggccgcga attc 284

<210> 18
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<400> 18

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1 5 10 15

Val Met Ala Pro Ala Ala Asp Arg Glu Gly Tyr Trp Gly Pro Thr Thr
20 25 30

Ser Thr Leu Asp Trp Cys Glu Glu Asn Tyr Ser Val Thr Trp Tyr Ile
35 40 45

Ala Glu Phe Trp Asn Thr Val Ser Asn Leu Ile Met Ile Ile Pro Pro
50 55 60

Met Phe Gly Ala Ile Gln Ser Val Arg Asp Gly Leu Glu Lys Arg Tyr
65 70 75 80

Ile Ala Ser Tyr Leu Ala Leu Thr Val Val Gly Met
85 90

<210> 19

<211> 928

<212> DNA

<213> Homo sapiens

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<221> modified_base

<222> (662)..(919)

<223> N = A, C, G or T/U

<400> 19

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ggatccgggtt ggaataagaa ctttcatcac cactgctgtc atctgtaaaa ctaggattgt 60
tatctgaata ttcatacaata gttgtaggtg tactactttc ctcaaaaatg cttcctctct 120
cactgtgact gtgtccattc attggccttag gtatagtctg gcttttaaga agatgtaaaa 180
gcaaactatt gtagcagct tgttttataat tgtttctttc cagtgaagttc ttataacctg 240
catttttagg ggaagaagga atgataccca ttggattttg aaacactgta gcactacttt 300
tgetagccat cagtttgctt gatgatgttc ttgcctgacc attaagatgg cttgacattc 360
cttttgagg ctggttaactg ccaacatcct tctggccatt ttcttgcaat ctggccatag 420
cagcaagtct ttcacttgct gcttgatttg cattttgctt ttttaaagcg tgttctcgag 480
aatactgctg caaatgggct tcgcttgaca gaagtaatgc taactggcta caagcaacac 540
taggtttaag tgaggtggca ggactagccc tttttccac catgcttgca acagcctgta 600
atcttgcagc acatgacaac gggtcactca tganccttgg tccactttgt ccacatgatg 660
angagactct gcaacctatc tctgatgang gtttttagtcn catcaggaan attcgaatca 720
ngcttttgac cttaacttta cttttctttc accaaagntt ttaagtggac tggagccaca 780
ccntagcacc ttaaaacctt ctcnctttt aaagaatctg gctggaggcc taatccttgn 840
ttccttgagg cttttgccng aattgggtgg gaccaaacca ccgnttgna accctaaacc 900
ttaaggactg gaaccaana aggccctt 928
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<210> 20

<211> 298

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES
 <222> (3)..(93)
 <223> XAA = ANYTHING

<400> 20

Gly	Ala	Xaa	Leu	Gly	Ser	Ser	Pro	Gly	Leu	Gly	Xaa	Pro	Xaa	Gly	Gly	1	5	10	15
Leu	Val	Pro	Thr	Asn	Ser	Gly	Lys	Ser	Leu	Lys	Glu	Xaa	Arg	Ile	Arg	20	25	30	
Pro	Pro	Ala	Arg	Phe	Phe	Lys	Lys	Xaa	Glu	Gly	Phe	Lys	Val	Leu	Xaa	35	40	45	
Cys	Gly	Ser	Ser	Pro	Leu	Lys	Xaa	Phe	Gly	Glu	Arg	Lys	Val	Lys	Leu	50	55	60	
Arg	Ser	Lys	Ala	Phe	Glu	Xaa	Ser	Xaa	Asp	Asn	Xaa	His	Gln	Arg	Val	65	70	75	80
Ala	Glu	Ser	Xaa	His	His	Val	Asp	Lys	Val	Asp	Gln	Xaa	Ser	Val	Thr	85	90	95	
Arg	Cys	His	Val	Leu	Gln	Asp	Tyr	Arg	Leu	Leu	Gln	Ala	Trp	Trp	Lys	100	105	110	
Lys	Gly	Leu	Val	Leu	Pro	Pro	His	Leu	Asn	Leu	Val	Leu	Leu	Val	Ala	115	120	125	
Ser	His	Tyr	Phe	Cys	Gln	Ala	Lys	Pro	Ile	Cys	Ser	Ser	Ile	Leu	Glu	130	135	140	
Asn	Thr	Leu	Lys	Arg	Lys	Met	Gln	Ile	Lys	Gln	Gln	Val	Lys	Asp	Leu	145	150	155	160
Leu	Leu	Trp	Pro	Asp	Cys	Lys	Lys	Met	Ala	Arg	Arg	Met	Leu	Ala	Val	165	170	175	
Thr	Ser	Ser	Gln	Lys	Glu	Cys	Gln	Ala	Ile	Leu	Met	Val	Arg	Gln	Glu	180	185	190	
His	His	Gln	Ala	Asn	Trp	Leu	Ala	Lys	Val	Val	Leu	Gln	Cys	Phe	Lys	195	200	205	
Ile	Gln	Trp	Val	Ser	Phe	Leu	Leu	Pro	Leu	Lys	Met	Gln	Val	Ile	Arg	210	215	220	
Thr	His	Trp	Lys	Glu	Thr	Ile	Asn	Lys	Leu	Leu	Thr	Ile	Val	Cys	Phe	225	230	235	240
Tyr	Ile	Phe	Leu	Lys	Ala	Arg	Leu	Tyr	Leu	Ser	Gln	Met	Asp	Thr	Val	245	250	255	
Thr	Val	Arg	Glu	Glu	Ala	Phe	Leu	Arg	Lys	Val	Val	His	Leu	Gln	Leu	260	265	270	

Leu Met Asn Ile Gln Ile Thr Ile Leu Val Leu Gln Met Thr Ala Val
 275 280 285

Val Met Lys Val Leu Ile Pro Thr Gly Ser
 290 295

<210> 21
 <211> 563
 <212> DNA
 <213> Homo sapiens

<400> 21
 ggatcctctt aggtctcgca ggctgtctat ggcttgctct ggtgatattg tgtcagacag 60
 gtatagtagg agacaagcag ctacaagaca agatctccca agtctccat agcagtgtat 120
 taagggtttt cggtaatttt taaggcagggt tgtaagctct tccattattt cacagcagct 180
 ggctatgtca ggagtccctc catctgcatg tggatgatga tgggtgataa ttccacattg 240
 ctggtagaga tccagaagggt ttgggactct atattttgac agttcccctc tgggtgcagaa 300
 aacaaatatg tcttgatata cacagctctt tagttcttct gtatcttttt ggacatttct 360
 tctaacatct ttaaattttac aacctggaag agcacataaa ccgagaaaact gagaacaatt 420
 cactcgtgac aaagatagcc atgatatatg aattggagtc tgttcatctt caataggctc 480
 ttcatctgat gagtcaaact cacttggttg tattgaactg ggcggcttca tcgctggccc 540
 gccgtcgacg cggccgcgaa ttc 563

<210> 22
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 22
 Ile Arg Gly Arg Val Asp Gly Gly Pro Ala Met Lys Pro Pro Ser Ser
 1 5 10 15
 Ile Gln Thr Ser Glu Phe Asp Ser Ser Asp Glu Glu Pro Ile Glu Asp
 20 25 30
 Glu Gln Thr Pro Ile His Ile Ser Trp Leu Ser Leu Ser Arg Val Asn
 35 40 45
 Cys Ser Gln Phe Leu Gly Leu Cys Ala Leu Pro Gly Cys Lys Phe Lys
 50 55 60
 Asp Val Arg Arg Asn Val Gln Lys Asp Thr Glu Glu Leu Lys Ser Cys
 65 70 75 80
 Gly Ile Gln Asp Ile Phe Val Phe Cys Thr Arg Gly Glu Leu Ser Lys
 85 90 95
 Tyr Arg Val Pro Asn Leu Leu Asp Leu Tyr Gln Gln Cys Gly Ile Ile
 100 105 110
 Thr His His His Pro Ile Ala Asp Gly Gly Thr Pro Asp Ile Ala Ser
 115 120 125

Cys Cys Glu Ile Met Glu Glu Leu Thr Thr Cys Leu Lys Asn Tyr Arg
 130 135 140

Lys Thr Leu Ile His Cys Tyr Gly Gly Leu Gly Arg Ser Cys Leu Val
 145 150 155 160

Ala Ala Cys Leu Leu Leu Tyr Leu Ser Asp Thr Ile Ser Pro Glu Gln
 165 170 175

Ala Ile Asp Ser Leu Arg Asp Leu Arg Gly Ser
 180 185

<210> 23

<211> 171

<212> DNA

<213> Homo sapiens

<400> 23

ggatcctgga tgccacgaga tggcaagagc cacaatcaat gaatgcatta tgggtcaaatac 60
 ttttcatgta tatggatgtg actatttttaa caaataaaaag aagtgaaaag ttaaaaaaaaaa 120
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa agtcgacgcg gccgcgaatt c 171

<210> 24

<211> 53

<212> PRT

<213> Homo sapiens

<400> 24

Glu Phe Ala Ala Ala Ser Thr Phe Phe Phe Phe Phe Phe Phe Phe Phe
 1 5 10 15

Phe Phe Phe Leu Thr Phe His Phe Phe Tyr Leu Leu Lys Ser His Pro
 20 25 30

Tyr Thr Lys Asp Leu Thr Ile Met His Ser Leu Ile Val Ala Leu Ala
 35 40 45

Ile Ser Trp His Pro
 50

<210> 25

<211> 678

<212> DNA

<213> Homo sapiens

<400> 25

ggatcctgca cttatccagg ttaagatcta aataggctgt aagtttcttg ttaaagtcac 60
 gaacaatgtt ggcaggatca ctatctgcaa actctgggac aggcacactg ataaattcaa 120
 cttcttcttc ttcaaagatt ttaatatctt cttcaattgt ctggtagaga gcagctgggg 180
 catctgcaga gggctcattt aagatgacat catctttgat gtactttatt ccacagtagt 240
 acacgtcatc tggttgaagt gcaaaatatt tgtacaagta tgctcctcct agaataacac 300

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ctgcaagcat aaatgctagt ccaaagcaca tgcaccaaca ccaggctctt ctttggccaa 360
ctggtaccac atcatctggg tccttgcaagt ccaccgcgac ggcgtcgggg gggatgatga 420
ggcctcctc gccgctcttg ggctcgtcct tcttggcctc cttctgggcc agagcggagt 480
tgaacgtcac cttcaccatg gcgcggcctg gggcgccctc gaagggcggc ggcggctcgg 540
ggcgcggtg cggctcccgg ctgcgattgc agcctctacg gncgggctcc gggagccggc 600
tncgggcggc tgaagaaggt cgggaagctt cgcggcggca gaagcggcta ctgcgggtcg 660
acgccggccg cgaaattc
678

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<210> 26
<211> 219
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (33)
<223> XAA = ANYTHING

```

```

<400> 26
Glu Phe Arg Gly Arg Arg Arg Pro Ala Val Ala Ala Ser Ala Ala Ala
 1             5             10             15

Lys Leu Pro Asp Leu Leu Gln Pro Pro Xaa Ala Gly Ser Arg Ser Pro
      20             25             30

Xaa Val Glu Ala Ala Ile Ala Ala Gly Ser Arg Ser Arg Ala Pro Ser
      35             40             45

Arg Arg Arg Pro Ser Arg Ala Pro Gln Ala Ala Pro Trp Arg Arg Ser
      50             55             60

Thr Pro Leu Trp Pro Arg Arg Arg Pro Arg Arg Thr Ser Pro Arg Ala
      65             70             75             80

Ala Arg Arg Arg Ser Ser Ser Pro Pro Thr Pro Ser Arg Trp Thr Ala
      85             90             95

Arg Thr Gln Met Met Trp Tyr Gln Leu Ala Lys Glu Glu Pro Gly Val
      100            105            110

Gly Ala Cys Ala Leu Asp His Leu Cys Leu Gln Val Leu Phe Glu Glu
      115            120            125

His Thr Cys Thr Asn Ile Leu His Phe Asn Gln Met Thr Cys Thr Thr
      130            135            140

Val Glu Ser Thr Ser Lys Met Met Ser Ser Met Ser Pro Leu Gln Met
      145            150            155            160

Pro Gln Leu Leu Ser Thr Arg Gln Leu Lys Lys Ile Leu Lys Ser Leu
      165            170            175

Lys Lys Lys Lys Leu Asn Leu Ser Val Cys Leu Ser Gln Ser Leu Gln
      180            185            190

```

Ile Val Ile Leu Pro Thr Leu Phe Met Thr Leu Thr Arg Asn Leu Gln
 195 200 205

Pro Ile Ile Leu Thr Trp Ile Ser Ala Gly Ser
 210 215

<210> 27

<211> 916

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (651)..(915)

<223> N = A, C, G, or T/U

<400> 27

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ggatcctagg acaaagccac atcccaaata cttgctgaga gcagtggcta caaatgttaa 60
catgagatta gacattgaga tggctccctt atattgagag aacatggact ttggagttgg 120
gcagacttga atttgcattc tggctctagt ggttactacc tagtgtggct ttgagctatt 180
aaactttcca aagtttcgaa ggacttatct gtaacatagt aatggtaatc caccttatgg 240
ggtagtgtgc ttgaagaggc tatttgggag gctgaggcaa gaggatcact tgaggccagg 300
agggtgaaac cagcctgggc aacacagcga gaccctgtgt ctacaaaaaa ttaaaaaatt 360
aggcattgtg gcgtgcacct gaagtcccag ctactcaagg cagagatggg aggatcactt 420
gtgcccagga gctccaggct gcagtgagcc atgattttgc cactgcactc cagactgggt 480
gacagagcaa gaccccttct ctttggtggg ggcaaaaaaa aaaaaaagag ggtatatgaa 540
gtacctagta taatatctag cctgaattgc ctataatgac gcacttcctt tctttccctt 600
ggggtttcagc tgncaaacac tcttctacaa gtaagataag cccagctttg natgggtcaat 660
ggataaacat ttcctatttc tttgtaaadc ccatnttctg cagacatctc aatttcacat 720
ttggccaaaa aagtcctttc attccttanc cctgganaaa taacctttnt taaatnttaa 780
accgntntgc ctgaactttg gctatcctct tntacatntc cttaaaccan ggacttggaa 840
cttcttggat cantcccaag attaattcct taantttttc anaccaaccg gtatgaagca 900
gggaatangg ccttnt
916

```

<210> 28

<211> 236

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (1)..(93)

<223> XAA = ANYTHING

<400> 28

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Xaa Gly Xaa Ile Pro Cys Phe Ile Pro Val Gly Xaa Lys Xaa Leu Arg
  1           5           10          15
Asn Ser Trp Xaa Ser Lys Lys Phe Gln Val Xaa Gly Leu Arg Xaa Cys
  20          25          30
Xaa Arg Gly Pro Lys Phe Arg Xaa Xaa Gly Leu Xaa Phe Xaa Lys Gly

```

35	40	45
Tyr Xaa Ser Arg Xaa Lys Glu Lys Asp Phe Phe Gly Gln Asn Asp Val		
50	55	60
Cys Arg Xaa Trp Asp Leu Gln Arg Asn Arg Lys Cys Leu Ser Ile Asp		
65	70	75 80
His Xaa Lys Leu Gly Leu Ser Tyr Leu Lys Ser Val Xaa Gln Leu Lys		
	85	90 95
Pro Lys Gly Lys Lys Gly Ser Ala Ser Leu Ala Ile Gln Ala Arg Tyr		
	100	105 110
Tyr Thr Arg Tyr Phe Ile Tyr Pro Leu Phe Phe Phe Phe Ala Pro Asn		
	115	120 125
Lys Glu Lys Gly Ser Cys Ser Val Thr Gln Ser Gly Val Gln Trp Gln		
	130	135 140
Asn His Gly Ser Leu Gln Pro Gly Ala Pro Gly His Lys Ser Ser His		
145	150	155 160
Leu Cys Leu Glu Leu Gly Leu Gln Val His Ala Thr Met Pro Asn Phe		
	165	170 175
Leu Ile Phe Cys Arg His Arg Val Ser Leu Cys Cys Pro Gly Trp Phe		
	180	185 190
Gln Pro Pro Gly Leu Lys Ser Ser Cys Leu Ser Leu Pro Asn Ser Leu		
	195	200 205
Phe Lys Thr Thr Thr Pro Gly Gly Leu Pro Leu Leu Cys Tyr Arg Val		
	210	215 220
Leu Arg Asn Phe Gly Lys Phe Asn Ser Ser Lys Pro		
225	230	235

<210> 29
 <211> 930
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (611)..(928)
 <223> N = A, C, G or T/U

<400> 29
 ggatccgtcg gactgcacgt tgtcatagaa tgtcaagtag ccaaaaatgg cagtcaagaa 60
 gtacataaca aacatggcga aaaaggagat gtttgaaacc atctgcattt ttttctgtga 120
 tcggtcttta agctcactgt aaattggcag gactgacggg tggcaaacia atgcaaatgc 180
 aatgggtgggt aaagcataca cggtctttga attgaaggta acatattttg gcgtacacgt 240
 gtcagcattt gttgaattag cacttattgt tgaatttagc tctggaacia tgcagggaat 300

```

ttgaaatttc ttgtaaataa ccacaattag gaaaaaaacc atacagctca aggaaaatcc 360
actagtatag ccaagatacc ctaagttctt caagagacac agagggagaa ttatgccaaa 420
ggtaactatc accaccagaa cgcggccatc cacgtaccag gctgaaaatg tctcttcctt 480
tcccattaga aacttttatgg cagagggtag ttcatTTTTT acgatgaaga ggtagctcag 540
cattgctcca gtgttctgta gagaggtggc ttcaaagatt acgaacttcc tgtggtgcc 600
aagacttggg nccccacttt tcatacacca tgcagnctgt tcttttgaac agatcaatag 660
ganggttaat ggaatatata gacagcaatg tcaactgaag caaaagtacc cgaaaaagtn 720
gggattccag tgtttgccag ggcaaaaggc caattcccaa aattccactt gnccataatg 780
gccttgctta aggttaaaac cgacatgcc taanggaggt tgnacctggg aatatactca 840
ttncactttt ttttttccaa aggctgtttg gganantttt tttanttttc cgaccnaaat 900
aaacttgnnt ttaacngacc tttttttnct
930

```

```

<210> 30
<211> 307
<212> PRT
<213> Homo sapiens

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```

<220>
<221> MOD_RES
<222> (1)..(104)
<223> XAA = ANYTHING

```

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<400> 30
Xaa Lys Lys Arg Ser Val Lys Xaa Lys Phe Ile Xaa Val Gly Lys Xaa
 1             5             10             15
Lys Lys Xaa Ser Gln Thr Ala Phe Gly Lys Lys Lys Val Xaa Val Tyr
      20             25             30
Ser Gln Val Gln Pro Pro Leu Gly His Val Gly Phe Asn Leu Lys Gln
      35             40             45
Gly His Tyr Gly Gln Val Glu Phe Trp Glu Leu Ala Phe Cys Pro Gly
 50             55             60
Lys His Trp Asn Pro Xaa Phe Phe Gly Tyr Phe Leu Gln His Cys Cys
 65             70             75             80
Leu Tyr Ile Pro Leu Thr Xaa Leu Leu Ile Cys Ser Lys Glu Gln Xaa
      85             90             95
Ala Trp Cys Met Lys Ser Gly Xaa Pro Ser Leu Trp His His Arg Lys
      100            105            110
Phe Val Ile Phe Glu Ala Thr Ser Leu Gln Asn Thr Gly Ala Met Leu
      115            120            125
Ser Tyr Leu Phe Ile Val Lys Asn Glu Leu Pro Ser Ala Ile Lys Phe
      130            135            140
Leu Met Gly Lys Glu Glu Thr Phe Ser Ala Trp Tyr Val Asp Gly Arg
      145            150            155            160
Val Leu Val Val Ile Val Thr Phe Gly Ile Ile Leu Pro Leu Cys Leu

```

165 170 175
 Leu Lys Asn Leu Gly Tyr Leu Gly Tyr Thr Ser Gly Phe Ser Leu Ser
 180 185 190
 Cys Met Val Phe Phe Leu Ile Val Val Ile Tyr Lys Lys Phe Gln Ile
 195 200 205
 Pro Cys Ile Val Pro Glu Leu Asn Ser Thr Ile Ser Ala Asn Ser Thr
 210 215 220
 Asn Ala Asp Thr Cys Thr Pro Lys Tyr Val Thr Phe Asn Ser Lys Thr
 225 230 235 240
 Val Tyr Ala Leu Pro Thr Ile Ala Phe Ala Phe Val Cys His Pro Ser
 245 250 255
 Val Leu Pro Ile Tyr Ser Glu Leu Lys Asp Arg Ser Gln Lys Lys Met
 260 265 270
 Gln Met Val Ser Asn Ile Ser Phe Phe Ala Met Phe Val Met Tyr Phe
 275 280 285
 Leu Thr Ala Ile Phe Gly Tyr Leu Thr Phe Tyr Asp Asn Val Gln Ser
 290 295 300
 Asp Gly Ser
 305

<210> 31
 <211> 919
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified base
 <222> (610)..(918)
 <223> N = A, C, G or T/U

<400> 31
 gggatccggg gattaaggat ggaggggacta aattcaagat attaacaaag gaacaaagaa 60
 acagggcctg atgggaggca gaggatagaa cagactgtac agtgggaata aagatcatatc 120
 ctatttataa ggaagtagaa aagacatggt aatggatata aaattgagtg tgaaacctgg 180
 gaaaggacag aaaactcctc ccttttgccct gacctccttt ttactcccct accttgccct 240
 gtgctatcct gagacactcc tcaattgctc aattaattct ccaggaaagg caaacctata 300
 gtcaatagtt agcttggaagaa gaatataggt taataattag agttggagga agctaacagt 360
 ggagatagga cttgagtagc tgccactggt agttttatct ataacctctc ctggaacctc 420
 gcattaacct cagatttcat tgaattaaaa agaagggtggg agggcaagta aatcaatcaa 480
 aacttcata aaacaagtac cccaactgaa ctaccatcaa ttaaagtga aactgcaggg 540
 gtatatgggt ggctggggct gaggccatct aaaggccaga ggggaaaaaa tgcataatgta 600
 taaatcagan gatgggtacc agaactgncc cttccttcaa tcagatcaca gcagagccca 660
 agatgcaggc aaccagtggg aaatcnttgg gaagactctg ggggtccaacc ccacgattag 720
 gggaaaccct tccttaaaaa gggttgcntga aggggaaact gggccctttg aaaaagttag 780
 nggaaccna gtggnccttg accttcacct tcggccatta ncttacaagg gaccttcctg 840

cnggggctg aaaattgcct cccatttta nctttaccta ggaacccctt ccnaggncaa 900
 tttgggttcc ccatggtnt 919

<210> 32
 <211> 290
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(100)
 <223> XAA = ANYTHING

<400> 32
 Xaa Pro Trp Gly Thr Gln Ile Xaa Leu Gly Arg Gly Ser Val Lys Xaa
 1 5 10 15
 Lys Trp Gly Gly Asn Phe Gln Ala Pro Ala Gly Arg Ser Leu Val Xaa
 20 25 30
 Trp Pro Lys Val Lys Val Lys Xaa His Xaa Gly Ser Xaa Asn Phe Phe
 35 40 45
 Lys Gly Pro Ser Phe Pro Phe Xaa Gln Pro Phe Gly Arg Val Ser Pro
 50 55 60
 Asn Arg Gly Val Gly Pro Gln Ser Leu Pro Xaa Asp Phe Pro Leu Val
 65 70 75 80
 Ala Cys Ile Leu Gly Ser Ala Val Ile Leu Lys Glu Gly Xaa Val Leu
 85 90 95
 Val Pro Ile Xaa Phe Ile His Met His Phe Phe Pro Ser Gly Leu Met
 100 105 110
 Ala Ser Ala Pro Ala Thr His Ile Pro Leu Gln Phe Ala Leu Leu Met
 115 120 125
 Val Val Gln Leu Gly Tyr Leu Phe Tyr Gly Ser Phe Asp Phe Thr Cys
 130 135 140
 Pro Pro Thr Phe Phe Leu Ile Gln Asn Leu Arg Leu Met Arg Gly Ser
 145 150 155 160
 Arg Arg Gly Tyr Arg Asn Tyr Gln Trp Gln Leu Leu Lys Ser Tyr Leu
 165 170 175
 His Cys Leu Pro Pro Thr Leu Ile Ile Asn Leu Tyr Ser Cys Gln Ala
 180 185 190
 Asn Tyr Leu Val Cys Leu Ser Trp Arg Ile Asn Ala Ile Glu Glu Cys
 195 200 205
 Leu Arg Ile Ala Gln Ala Lys Val Gly Glu Lys Gly Gly Gln Ala Lys

<223> XAA = ANYTHING

<400> 34

Xaa Asn Xaa Val Pro Xaa Leu Gly Xaa Ser Xaa Phe Xaa Xaa Xaa Xaa
1 5 10 15
Gln Xaa Xaa Xaa Xaa Pro Xaa Leu Xaa Lys Xaa Xaa Ala Phe Xaa Lys
20 25 30
Xaa Xaa Gly Xaa Xaa Gly Pro Gly Xaa Pro Xaa Lys Lys Trp Ala Xaa
35 40 45
Xaa Leu Asp Arg Val Thr Ser Ser Xaa Lys Xaa Ser Arg Arg Ile Cys
50 55 60
Trp Ala Thr Gln Met His Ser Asn Leu Met Asn Val Ile Leu Ser Glu
65 70 75 80
Val Ser Trp Arg Ile Trp Ser Leu Arg Ile Cys Gln Met Ala Leu Ser
85 90 95
Leu Pro Tyr Pro Phe Arg Xaa Ser Thr Phe Leu Met Met Lys Ile Arg
100 105 110
Leu Gly Gln Pro Lys Leu Cys Tyr Val Ser Arg Ile Pro Thr Ile Trp
115 120 125
Ile Gln Ile Pro Ser Gln Arg Val Ile Phe Gln Glu Asn Thr Asn Leu
130 135 140
Phe Arg Ala Glu Asp Cys Phe Glu Leu Gly Lys Val Ala Tyr Thr Glu
145 150 155 160
Ala Asp Tyr Tyr His Thr Glu Leu Trp Met Glu Gln Ala Leu Arg Gln
165 170 175
Leu Asp Glu Gly Glu Ile Ser Thr Ile Asp Lys Val Ser Val Leu Asp
180 185 190
Tyr Leu Ser Tyr Ala Val Tyr Gln Gln Gly Asp Leu Asp Lys Ala Leu
195 200 205
Leu Leu Thr Lys Lys Leu Leu Glu Leu Asp Pro Glu His Gln Arg Ala
210 215 220
Asn Gly Asn Leu Lys Tyr Phe Glu Tyr Ile Met Ala Lys Glu Lys Asp
225 230 235 240
Val Asn Lys Ser Ala Ser Asp Asp Gln Ser Asp Gln Lys Thr Thr Pro
245 250 255
Lys Lys Lys Gly Val Ala Val Asp Tyr Leu Pro Glu Arg Gln Lys Tyr
260 265 270
Glu Met Leu Cys Arg Gly Glu Gly Ile Lys Met Thr Pro Arg Arg Gln

275

280

285

Lys Lys Leu Phe Cys Arg Tyr His Gly Gly Ser
290 295

<210> 35

<211> 916

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (735)..(915)

<223> N = A, C, G, OR T/U

<400> 35

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ctccccacgg cacagcattt cgtacttctg tctctctggc aggtaatcca cagcaacccc 120
ttttttcttt ggtgtagttt tctgatcaga ttggtcatct gaagcagact tattgacatc 180
tttttcttta gccattatat actcaaaata ttttaagtta ccattagctc tctgatgttc 240
aggatctagt tcaagaagct tctttgtgag caaaagtgcc ttatccaggt ctccctgctg 300
atataccgca tagctcaaat aatctagaac agagacttta tctatggtag aaatctcgcc 360
ttcatccagt tgccttaggg cttgttccat ccacagttcc gtatggtaat aatctgcttc 420
tgtataggcc actttgccca actcaaagca gtcctcagcc cgttagaaaa gatttggtgtt 480
tcactcctgg aagattaccc tttgagatgg tatctgtatc caaattgtag gtatcctgga 540
gacgtaacag agctttggct gcccacacct gatcttcac ctaggaaag tactgnctct 600
gaatgggtan ggtagagata aagccatctg acatatcctt aaggaccaga ttctccaact 660
cacttcactc agtattcaga cgttcattaa atttgaatgc atttactggg tggcccaaca 720
aatccttctg gaacntttgn cgctggacta agttaccoga tctaacttct ntgcccattt 780
tttaantggn ctacctgggc cntntggcc ttaannnanc tttcnaaaag cccnnaactt 840
tncaagnntg ggcnaannng ncntttgccn ntgannnaaa aacntggang nccccaanct 900
gggaaccnaa ttnnnt 916

```

<210> 36

<211> 106

<212> PRT

<213> Homo sapiens

<400> 36

```

Asn Ser Arg Pro Arg Arg Pro Gly Trp Leu Arg Gly Ala Ala Pro Gly
 1           5           10          15
Pro Arg Gly Ser Gln Ser Asn Glu Thr Thr Ala Cys Ser Arg Leu Val
      20           25           30
Glu Ile Ser Arg Arg His Gln Trp Ala Arg Ser Glu Pro Ser Gly Pro
      35           40           45
Pro Val Trp Asn Gln Thr Cys Ala Arg Gly Arg Ala Val Gly Gln Arg
      50           55           60
Gly Arg Gly Asp Glu Gly Ala Met Ala Arg Lys Leu Ser Val Ile Leu
      65           70           75           80

```

Ile Leu Thr Phe Ala Leu Ser Val Thr Asn Pro Leu His Glu Leu Lys
85 90 95

Ala Ala Ala Phe Pro Gln Thr Thr Gly Ser
100 105

<210> 37

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (586)

<223> N = A, C, G, OR T/U

<400> 37

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ggatccacca accccggcct cccaaagtgc tgggattaca ggcattgagcc accacgcca 60
gccattcctt gtcatttcta tcatttgata catctatact tctgaataat cataactgat 120
actcaaagag atgccctgac accctccaag gttctacaag gtgaccaaata cagagagggtc 180
acctcatgcc tagtattatt ttgggggttag catacatttt ataataatta ttttaaaact 240
ggcaatccat tttgggactc aatgacagct ctctctatta atcatattgt tttattaact 300
gaaatagtcc actcagtcag taggattaat gatcagagat tatgacacaa ctaaaaccaa 360
agctgggggca atgggctctc agaatggaac caccattat gaactatcca tctgaccaac 420
tctttaactt tcttcctaaa tatgagatca ccaaggcgtt tcaatgcagc ctgcacaatt 480
catggggcag ggtcctcaga ttaaagactt tacatttatg tagaattcaa gtatcatttt 540
tcactaagca aactctattt gctcactctc ttctacatgt aattgnccaa ctttggttga 600
ctgctgagtc ctcatgggaa gaattc 626

```

<210> 38

<211> 188

<212> PRT

<213> Homo sapiens

<400> 38

```

Ile Leu Pro Met Arg Thr Gln Gln Ser Thr Lys Val Gly Gln Leu His
 1           5           10           15

Val Glu Glu Ser Glu Gln Ile Glu Phe Ala Lys Met Ile Leu Glu Phe
 20           25           30

Tyr Ile Asn Val Lys Ser Leu Ile Gly Pro Cys Pro Met Asn Cys Ala
 35           40           45

Gly Cys Ile Glu Thr Pro Trp Ser His Ile Glu Glu Ser Arg Val Gly
 50           55           60

Gln Met Asp Ser Ser Trp Val Val Pro Phe Glu Pro Ile Ala Pro Ala
 65           70           75           80

Leu Val Leu Val Val Ser Ser Leu Ile Ile Asn Pro Thr Asp Val Asp
 85           90           95

```

Tyr Phe Ser Asn Asn Met Ile Asn Arg Glu Ser Cys His Val Pro Lys
 100 105 110
 Trp Ile Ala Ser Phe Lys Ile Ile Ile Lys Cys Met Leu Thr Pro
 115 120 125
 Lys Tyr Ala Gly Asp Leu Ser Asp Leu Val Thr Leu Asn Leu Gly Gly
 130 135 140
 Cys Gln Gly Ile Ser Leu Ser Ile Ser Tyr Asp Tyr Ser Glu Val Met
 145 150 155 160
 Tyr Gln Met Ile Glu Met Thr Arg Asn Gly Trp Ala Trp Trp Leu Met
 165 170 175
 Pro Val Ile Pro Ala Leu Trp Glu Ala Gly Val Gly
 180 185

<210> 39
 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (634)..(896)
 <223> N = A, C, G OR T/U

<400> 39
 ggatcctgag ctaagcatgg tccctccgta gatatccaga gccagctgag aataggcaaa 60
 gccaaaaaca gtgatggtca ggccggccag cagggccagc ttgagcaggg actccaagac 120
 tgcagcagcc acagcaacgt cctcctgctt ctgaagtgtg gcatcctttc ccctctccag 180
 caccttagca aaaaatatat aaaaactttc ctctattggc tggaaaatta atctggccac 240
 aaggagacca agattattca ctatatcata cacaccctga tcaccaaagt tcaatacatt 300
 caaaaatgtc atcacatatc gctcgcttct tgtcaaaatc tgtttcaaga aagactgttt 360
 gaaaaaactc caagtcagtt tagcctcttt ccagtttata aacgctccat ttcttgaat 420
 attgggtaac agatctgtta ttctggagac aggaagagtt tgaagcttgg ttgattctgg 480
 ggaaccaggt aactttgtga aataaataac atagcagagc accagaactg tggatatagaa 540
 aagctgggcc aaagagaaaa tgtacaatcc ccagtgaagg aaccacagca cgagaaaagc 600
 tgtcagacgc tcttaagaat taccgcaggc tctntgcaat caccttgagc ttncaaacat 660
 atgtgcttgt gcccaagaac caaaaggctn ttctanaagc ttcaccactg gcgaaagacc 720
 aaccgnacca ntccagttgc atantgaggg acaccattag gatcngcctt tnagcagttt 780
 aaccagatcn gcccaggaat anggcccaac ttcccagggg actgttacct ancaggttaa 840
 gggctggtcc agctnccctgg ggccccctgg anatgtttgn gaaggccttt ggccnnt 897

<210> 40
 <211> 296
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES

<222> (1)..(86)

<223> XAA = ANYTHING

<400> 40

Xaa Gly Gln Arg Pro Ser Gln Thr Xaa Pro Gly Gly Pro Arg Xaa Leu
1 5 10 15

Asp Gln Pro Leu Thr Xaa Trp Val Thr Val Pro Trp Glu Val Gly Pro
20 25 30

Tyr Ser Trp Ala Asp Leu Val Xaa Leu Leu Lys Gly Xaa Ser Trp Cys
35 40 45

Pro Ser Xaa Cys Asn Trp Xaa Gly Xaa Val Gly Leu Ser Pro Val Val
50 55 60

Lys Leu Xaa Glu Xaa Pro Phe Gly Ser Trp Ala Gln Ala His Met Phe
65 70 75 80

Xaa Ser Ser Arg Leu Xaa Arg Ala Cys Gly Asn Ser Glu Arg Leu Thr
85 90 95

Ala Phe Leu Val Leu Trp Leu Pro His Trp Gly Leu Tyr Ile Phe Ser
100 105 110

Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu Val Leu Cys Tyr Val Ile
115 120 125

Tyr Phe Thr Lys Leu Leu Gly Ser Pro Glu Ser Thr Lys Leu Gln Thr
130 135 140

Leu Pro Val Ser Arg Ile Thr Asp Leu Leu Pro Asn Ile Thr Arg Asn
145 150 155 160

Gly Ala Phe Ile Asn Trp Lys Glu Ala Lys Leu Thr Trp Ser Phe Phe
165 170 175

Lys Gln Ser Phe Leu Lys Gln Ile Leu Thr Glu Gly Glu Arg Tyr Val
180 185 190

Met Thr Phe Leu Asn Val Leu Asn Phe Gly Asp Gln Gly Val Tyr Asp
195 200 205

Ile Val Asn Asn Leu Gly Ser Leu Val Ala Arg Leu Ile Phe Gln Pro
210 215 220

Ile Glu Glu Ser Phe Tyr Ile Phe Phe Ala Lys Val Leu Glu Arg Gly
225 230 235 240

Lys Asp Ala Thr Leu Gln Lys Gln Glu Asp Val Ala Val Ala Ala Ala
245 250 255

Val Leu Glu Ser Leu Leu Lys Leu Ala Leu Leu Ala Gly Leu Thr Ile
260 265 270

Thr Val Phe Gly Phe Ala Tyr Ser Gln Leu Ala Leu Asp Ile Tyr Gly
 275 280 285

Gly Thr Met Leu Ser Ser Gly Ser
 290 295

<210> 41
 <211> 607
 <212> DNA
 <213> Homo sapiens

<400> 41
 ggatccgtgg ccagaaaaaa aaaaatcggt acctacaaaa tctcttgggc aacacttaag 60
 ccatggaaga gccacatga atccaggtct actttccttt acaggtagat tccagaacaa 120
 caacaaaaaa tgtaagacta caagaaatga tttaatatga taaaactccc atttcaaaac 180
 ccagttctaa aggatttacn tgactaatgc ntgattatgt agtcatggaa aatgtctctc 240
 ataaaagtgc tcctaacaaa acatgatcta caataattta taaaatgtga agggttggga 300
 tgtgcagact gattgggtgc cgtcaggttg tttctcttaa ataaggata aaaaactatg 360
 atatcatagt ctttcgactt tattttctga gataaaaaag tataggcata ggtgttttta 420
 atagtcttct tgatgatatc ctttagaata atctatcaaa tggcttcttt catgtttcct 480
 gattatcagc attcatcagt gttactgtca gccttgatta agtggttgaa aatttcagag 540
 aagaataagc aacttctgtg aacctttccc caatccctga gaatcatgtc gacgcggccg 600
 cgaattc 607

<210> 42
 <211> 189
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (121)
 <223> XAA = ANYTHING

<400> 42
 Asn Ser Arg Pro Arg Arg His Asp Ser Gln Gly Leu Gly Lys Gly Ser
 1 5 10 15
 Gln Lys Leu Leu Ile Leu Leu Asn Phe Gln Pro Leu Asn Gln Gly Gln
 20 25 30
 His Met Leu Ile Ile Arg Lys His Glu Arg Ser His Leu Ile Asp Tyr
 35 40 45
 Ser Lys Gly Tyr His Gln Glu Asp Tyr Lys His Leu Cys Leu Tyr Phe
 50 55 60
 Phe Ile Ser Glu Asn Lys Val Glu Arg Leu Tyr His Ser Phe Leu Tyr
 65 70 75 80
 Leu Ile Glu Lys Gln Pro Asp Val His Gln Ser Val Cys Thr Ser Gln
 85 90 95

Pro Phe Thr Phe Tyr Lys Leu Leu Ile Met Phe Cys Glu His Phe Tyr
100 105 110

Glu Arg His Phe Pro Leu Asn Asn Xaa Ala Leu Val Xaa Ile Leu Asn
115 120 125

Trp Val Leu Lys Trp Glu Phe Tyr His Ile Lys Ser Phe Leu Val Val
130 135 140

Leu His Phe Leu Leu Leu Phe Trp Asn Leu Pro Val Lys Glu Ser Arg
145 150 155 160

Pro Gly Phe Met Trp Ala Leu Pro Trp Leu Lys Cys Cys Pro Arg Asp
165 170 175

Phe Val Gly Asn Asp Phe Phe Phe Ser Gly His Gly Ser
180 185

<210> 43
<211> 466
<212> DNA
<213> Homo sapiens

<400> 43
ggatccttta atgtcctcat ttgttgctctg gttggagctg atcaagtagg tgtggaatcc 60
tgagaggcca acgatggacc agacagagaa gaagcacacc acagcctcca ggacgcttgc 120
aggactgtcc ttaagggcat ttaggaatcc tgtttgctgt gaacgaagaa tgacgtgggt 180
gataacgaat gcaaataataa agactgtcag aaaagacaga gataaaataa acatataaaa 240
aaatctgtag tttcttttcc ccacacagtt gcctaccag ggacagtggg gatcaaaccg 300
ttctacgcag ttatcacaaa ggctgcaatg ggaggcgcgga gggggccgga aaatcttgca 360
ggtgaaacag tatttaagtt tcacggtctg gccattgatg atgacttctt tggttctggg 420
aggcgggcgg taccctccctg aactgggtcg acgcggccgc gaattc 466

<210> 44
<211> 153
<212> PRT
<213> Homo sapiens

<400> 44
Asn Ser Arg Pro Arg Arg Pro Ser Ser Gly Gly Tyr Arg Pro Pro Pro
1 5 10 15

Arg Thr Lys Glu Val Ile Ile Asn Gly Gln Thr Val Lys Leu Lys Tyr
20 25 30

Cys Phe Thr Cys Lys Ile Phe Arg Pro Pro Arg Ala Ser His Cys Ser
35 40 45

Leu Cys Asp Asn Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val
50 55 60

Gly Asn Cys Val Gly Lys Arg Asn Tyr Arg Phe Phe Tyr Met Phe Ile
65 70 75 80

Leu Ser Leu Ser Phe Leu Thr Val Phe Ile Phe Ala Phe Val Ile Thr
85 90 95

His Val Ile Leu Arg Ser Gln Gln Thr Gly Phe Leu Asn Ala Leu Lys
100 105 110

Asp Ser Pro Ala Ser Val Leu Glu Ala Val Val Cys Phe Phe Ser Val
115 120 125

Trp Ser Ile Val Gly Leu Ser Gly Phe His Thr Tyr Leu Ile Ser Ser
130 135 140

Asn Gln Thr Thr Asn Glu Asp Ile Lys
145 150

<210> 45

<211> 395

<212> DNA

<213> Homo sapiens

<400> 45

ggatcctgtg acaatctgat ggccatacca ggagcaagct accaaggcgg caagacctgc 60
cacgatgaaa attatgcctc caccatggc tatacgggcc ttcttcactt tgcgtctctcc 120
cccacagcgc agtgcacttc atgccatcg tggccacaaa catggccagg aagcccagca 180
ccagggagac caccattagg gctcgagtgg cctgcaaggc cgcggacagg gcgagcaccg 240
agtcgtacat tttgcagctc atcatccccg tgctctgcgt gacgcagtcc atccacagcc 300
ccttgtagat ggcctggggc gtgatgatgt tgcacccgc ataggagctc atctgccact 360
gcgggatggc ggtgcgtcga cgcggccgcg aattc 395

<210> 46

<211> 126

<212> PRT

<213> Homo sapiens

<400> 46

Ile Arg Gly Arg Val Asp Ala Pro Pro Ser Arg Ser Gly Arg Ala Pro
1 5 10 15

Met Arg Val Thr Thr Ser Ser Arg Pro Arg Pro Cys Thr Arg Gly Cys
20 25 30

Gly Trp Thr Ala Ser Arg Arg Ala Arg Gly Ala Ala Lys Cys Thr Thr
35 40 45

Arg Cys Ser Pro Cys Pro Arg Pro Cys Arg Pro Leu Glu Pro Trp Trp
50 55 60

Ser Pro Trp Cys Trp Ala Ser Trp Pro Cys Leu Trp Pro Arg Trp Ala
65 70 75 80

Ser Ala Leu Arg Cys Gly Gly Asp Asp Lys Val Lys Lys Ala Arg Ile
85 90 95

Ala Met Gly Gly Gly Ile Ile Phe Ile Val Ala Gly Leu Ala Ala Leu
 100 105 110

Val Ala Cys Ser Trp Tyr Gly His Gln Ile Val Thr Gly Ser
 115 120 125

<210> 47
 <211> 597
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (7)..(594)
 <223> N = A, C, G OR T/U

<400> 47
 ggatccnanc tncnnacacn nacagagatc gacgnnnnct accaggtgag ccattgcggt 60
 aatatggact ttattnaagt aagttactta tattactgcc ttnccataca ctatntaatn 120
 ncatttgaat tactgagaga ctaatatgcc atgtctaaaa ctgtctcttt cataagtaat 180
 tttgngcctn cngctacnec aagcnaagnc aactcttcct tttttatata ctatganatg 240
 gcnccgangg cgaggagaan gctgaangnc tncgaactgg cagcggngan accgganngn 300
 acnangaagc gggnnncccn ttgcgngcca nnntcttttg nnttatcacg gnnagccanc 360
 gctnnggnct gatagcgntc cgncncaccc agccggccan agtcgatgaa tccnaaaaag 420
 cggccatttt ccaccatgan attcggcaag caggcatcgc catgggtcac gacganatcc 480
 tcgccgncgg gcatgcncgc cttgagcctg gcgaacagtt cggntggcgc gagcccctga 540
 tgctnttcgn ccaaatacgc ctgatcgaca agaccggctt ccacccgagn acgngct 597

<210> 48
 <211> 192
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (2)..(192)
 <223> XAA = ANYTHING

<400> 48
 Ser Xaa Xaa Ser Asp Gly Ser Arg Ser Cys Arg Ser Gly Phe Gly Arg
 1 5 10 15
 Xaa Ala Ser Gly Ala Arg Ala Xaa Arg Thr Val Arg Gln Ala Gln Gly
 20 25 30
 Xaa His Ala Arg Arg Arg Gly Xaa Arg Arg Asp Pro Trp Arg Cys Leu
 35 40 45
 Leu Ala Glu Xaa His Gly Gly Lys Trp Pro Leu Phe Xaa Ile His Arg
 50 55 60
 Leu Trp Pro Ala Gly Xaa Xaa Gly Xaa Leu Ser Xaa Xaa Ser Xaa Gly

65	70	75	80
Xaa Pro Xaa Gln Arg Xaa Trp Xaa Arg Xaa Gly Xaa Pro Leu Xaa Xaa	85	90	95
Xaa Xaa Arg Xaa Xaa Arg Cys Gln Phe Xaa Xaa Xaa Gln Xaa Ser Pro	100	105	110
Arg Xaa Arg Xaa His Xaa Ile Val Tyr Lys Lys Gly Arg Val Xaa Xaa	115	120	125
Ala Ser Xaa Ser Xaa Arg Xaa Lys Ile Thr Tyr Glu Arg Asp Ser Phe	130	135	140
Arg His Gly Ile Leu Val Ser Gln Phe Lys Xaa Xaa Xaa Ile Val Tyr	145	150	155
Gly Lys Ala Val Ile Val Thr Tyr Xaa Asn Lys Val His Ile Thr Ala	165	170	175
Met Ala His Leu Val Xaa Xaa Val Asp Leu Cys Xaa Cys Xaa Xaa Xaa	180	185	190

<210> 49
 <211> 547
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (538)
 <223> N = A, C, G OR T/U

<400> 49
 ggatccccac aaacacacag gactccctcc ctcccacaga gaacacaaaag ttgttaactg 60
 aagaacaaga taaataatat gctagtccat tttactgatt ttaaagatac tgcaattttt 120
 atacatttcg atgatttttc aacattttgc agctgtttgg ctttgcagca cagcaattca 180
 tacactatac ntgtacaaaa ttaccagcaa gactggaatg atgtattaat agaaggcacc 240
 atcatgctta ttacattacc agagaacaaa aatacagtaa agacaatttt cactgtacac 300
 agcttaaaga aaggaaaaaa ggggaggagg agtgtgttga gcagccagcc atccctgtac 360
 tgaagagggg caggtagaaa aatccttagat atggagctac taaatctggt ctaatagtca 420
 agaccatcgc atttgaagtt ctaattttta ttatttagtt cataactaaa atgatttcct 480
 tctggaatat acttgtagtc ttgttaaggt ttatgtgtac acacgctgtc gacgcggncg 540
 cgaattc 547

<210> 50
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 50

Asn Ser Arg Pro Arg Arg Gln Arg Val Tyr Thr Thr Leu Thr Arg Leu
1 5 10 15

Gln Val Tyr Ser Arg Arg Lys Ser Phe Leu Thr Lys Lys Leu Glu Leu
20 25 30

Gln Met Arg Trp Ser Leu Leu Asp Gln Ile Leu His Ile Asp Phe Ser
35 40 45

Thr Cys Pro Ser Ser Val Gln Gly Trp Leu Ala Ala Gln His Thr Pro
50 55 60

Pro Pro Leu Phe Ser Phe Leu Ala Val Tyr Ser Glu Asn Cys Leu Tyr
65 70 75 80

Cys Ile Phe Val Leu Trp Cys Asn Lys His Asp Gly Ala Phe Tyr Tyr
85 90 95

Ile Ile Pro Val Leu Leu Val Ile Leu Tyr Xaa Tyr Ser Val Ile Ala
100 105 110

Val Leu Gln Ser Gln Thr Ala Ala Lys Cys Lys Ile Ile Glu Met Tyr
115 120 125

Lys Asn Cys Ser Ile Phe Lys Ile Ser Lys Met Asp His Ile Ile Tyr
130 135 140

Leu Val Leu Gln Leu Thr Thr Leu Cys Ser Leu Trp Glu Gly Gly Ser
145 150 155 160

Pro Val Cys Leu Trp Gly Ser
165

<210> 51

<211> 742

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (512)..(741)

<223> N = A, C, G OR T/U

<400> 51

ggatcctgag tcaagccaaa aaaaaaaaaa aaacccaaaac aaaacaaaaa aaacaaataa 60
agccatgcc aatctcatctt gttttctgcg caagttaggt tttgtcaaga aaggggtgtaa 120
cgcaacttaa gtcatagtcc gcctagaagc atttgcggtg gacgatggag gggccggact 180
cgtcatactc ctgcttgctg atccacatct gctggaaggt ggacagcgag gccaggatgg 240
agccgccgat ccacacggag tacttgcgct caggaggagc aatgatcttg atcttcattg 300
tgctgggtgc cagggcagtg atctccttct gcacacctgc ggcaatgcc gggatcatgg 360
tggtgccgcc agacagcact gtgttgccgt acaggtcttt gcggatgtcc acgtcacact 420
tcatgatgga gttgaaggta gtttcgtgga tgccacagga ctccatgccc aggaaggaag 480
gctggaagag tgcctcaggg cagcggaacc gntcattgcc aatggtgatg acctggccgt 540

```

caggcancct cgtanctctt ctncagggag gagctggaan cagccgtggc catttcttgc 600
tcgaagtcca gcgncgacgt accnntaccn tntccttant gcctaccccn cgatttcccc 660
gtcgcgtcgn nntngtcenn ancnntccc centtcttg nncgnntnct cnnnngcgcn 720
nncgncngn ntcnncttn nt 742

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<210> 52
<211> 243
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (1)..(62)
<223> XAA = ANYTHING

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<400> 52
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Glu Xaa Xaa Xaa Xaa Glu
 1                5                10                15
Xaa Gly Xaa Xaa Xaa Gly Xaa Xaa Arg Xaa Ser Gly Glu Ile Xaa Gly
                20                25                30
Ala Xaa Arg Xaa Xaa Xaa Xaa Tyr Val Xaa Ala Gly Leu Arg Ala Arg
                35                40                45
Asn Gly His Gly Xaa Phe Gln Leu Leu Pro Xaa Glu Glu Xaa Arg Gly
                50                55                60
Cys Leu Thr Ala Arg Ser Ser Pro Leu Ala Met Xaa Gly Ser Ala Ala
                65                70                75                80
Leu Arg His Ser Ser Ser Leu Pro Ser Trp Ala Trp Ser Pro Val Ala
                85                90                95
Ser Thr Lys Leu Pro Ser Thr Pro Ser Ser Val Thr Trp Thr Ser Ala
                100                105                110
Lys Thr Cys Thr Pro Thr Gln Cys Cys Leu Ala Ala Pro Pro Cys Thr
                115                120                125
Leu Ala Leu Pro Thr Gly Cys Arg Arg Arg Ser Leu Pro Trp His Pro
                130                135                140
Ala Gln Arg Ser Arg Ser Leu Leu Leu Leu Ser Ala Ser Thr Pro Cys
                145                150                155                160
Gly Ser Ala Ala Pro Ser Trp Pro Arg Cys Pro Pro Ser Ser Arg Cys
                165                170                175
Gly Ser Ala Ser Arg Ser Met Thr Ser Pro Ala Pro Pro Ser Ser Thr
                180                185                190
Ala Asn Ala Ser Arg Arg Thr Met Thr Val Ala Leu His Pro Phe Leu
                195                200                205

```

Thr Lys Pro Asn Leu Arg Arg Lys Gln Asp Glu Ile Gly Met Ala Leu
 210 215 220

Phe Val Phe Phe Val Leu Phe Trp Phe Phe Phe Phe Phe Trp Leu Asp
 225 230 235 240

Ser Gly Ser

<210> 53
 <211> 598
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (214)..(597)
 <223> N = A, C, G OR T/U

<400> 53
 ggatcctttc actgagtatt tgtcagggtc acactgggtg caagaagttt ctcctttatt 60
 tgaataagag ttggctgggc aaagtttgca gaaagaggag ccctgcttgt ctgcatacgt 120
 gccaggtttg caggggaagc attctgaagt gtaggccacc cctgttatgg caatgtttct 180
 caccagcaca ggcttgggta ctttgggtcca tacntgagaa ggctgtgggt ctccaataga 240
 ggacattatt gcttcgattt agctccacac tgtggaattc ccatectttc tctgtggtct 300
 tcatccacct ggagtcattt gcattgggct ggcactggtc attctgaacg aaaaactcaa 360
 agatgatgct ggagtcctgga tagtagtatt cgaagttaac ggtgccagat tgcttcagggt 420
 tgacggcgta catcagtggt gctgtgcatt cgtccgtgtt ggaggcgatg tagtcgcccc 480
 ggggaaccca cttggacgaa gtacagttcc cgggtggactc agcagcactg tcatccagct 540
 ccatgntggc tgagaggctg gcanagccat gggncanntc atcccactca tcanacnc 598

<210> 54
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(124)
 <223> XAA = ANYTHING

<400> 54
 Xaa Xaa Met Ser Gly Met Xaa Xaa Pro Met Ala Xaa Pro Ala Ser Gln
 1 5 10 15

Pro Xaa Trp Ser Trp Met Thr Val Leu Leu Ser Pro Pro Gly Thr Val
 20 25 30

Leu Arg Pro Ser Gly Phe Pro Gly Ala Thr Thr Ser Pro Pro Thr Arg
 35 40 45

Thr Asn Ala Gln Pro His Cys Thr Pro Ser Thr Ser Asn Leu Ala Pro

50

55

60

Leu Thr Ser Asn Thr Thr Ile Gln Thr Pro Ala Ser Ser Leu Ser Phe
65 70 75 80

Ser Phe Arg Met Thr Ser Ala Ser Pro Met Gln Met Thr Pro Gly Gly
85 90 95

Arg Pro Gln Arg Lys Asp Gly Asn Ser Thr Val Trp Ser Ile Glu Ala
100 105 110

Ile Met Ser Ser Ile Gly Glu Pro Gln Pro Ser Xaa Val Trp Thr Lys
115 120 125

Val Pro Lys Pro Val Leu Val Arg Asn Ile Ala Ile Thr Gly Val Ala
130 135 140

Tyr Thr Ser Glu Cys Phe Pro Cys Lys Pro Gly Thr Tyr Ala Asp Lys
145 150 155 160

Gln Gly Ser Ser Phe Cys Lys Leu Cys Pro Ala Asn Ser Tyr Ser Asn
165 170 175

Lys Gly Glu Thr Ser Cys His Gln Cys Asp Pro Asp Lys Tyr Ser Val
180 185 190

Lys

<210> 55

<211> 657

<212> DNA

<213> Homo sapiens

<400> 55

ggatcccatg aggtagtcgg tcaggtcccg gccagccagg tccagacgca ggatggcgtg 60
ggggagggcg tagccctcgt agatgggcac cgtgtgggtg acccgcgtctc cagagtccat 120
gacaatgcca gtggtgcgcc cagaggcgta gagggacagc acggcctgga tggccacgta 180
catggccggg gtgttgagg tctcaaacat aatctgagtc atcttctctc tgttggcctt 240
ggggttcagg ggggcctcgg tcagcagcac tgggtgctcc tccggggcca cgcgcagctc 300
gtttagaag gtgtggtgcc agatcttctc catgtcgtcc cagttggtga cgatgccatg 360
ctcaatgggg tacttcaggg tcaggatgcc acgcttgctc tgggcctcgt cgccacgta 420
ggagtccttc tggcccatgc ccaccatgac gccctgggtg ctggggcgcc cgacgatgga 480
aggaaacacg gctcggggag cgtcgtcccc agcaaaacca gctttgcaca tgccggagcc 540
attgtcaatg accagcgcgg cgatctcttc ttccattgcg accggcagag aaacgcgcgg 600
cggagcggcg gaagaacaga gtgcgagagt tggcagcgtc gacgcggccg cgaattc 657

<210> 56

<211> 219

<212> PRT

<213> Homo sapiens

<400> 56

Glu Phe Ala Ala Ala Ser Thr Leu Pro Thr Leu Ala Leu Cys Ser Ser
 1 5 10 15
 Ala Ala Pro Pro Arg Val Ser Leu Pro Val Ala Met Glu Glu Glu Ile
 20 25 30
 Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met Cys Lys Ala Gly Phe
 35 40 45
 Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro Ser Ile Val Gly Arg
 50 55 60
 Pro Arg His Gln Gly Val Met Val Gly Met Gly Gln Lys Asp Ser Tyr
 65 70 75 80
 Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile Leu Thr Leu Lys Tyr
 85 90 95
 Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp Asp Met Glu Lys Ile
 100 105 110
 Trp His His Thr Phe Tyr Asn Glu Leu Arg Val Ala Pro Glu Glu His
 115 120 125
 Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu
 130 135 140
 Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn Thr Pro Ala Met Tyr
 145 150 155 160
 Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr
 165 170 175
 Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr His Thr Val Pro Ile
 180 185 190
 Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala
 195 200 205
 Gly Arg Asp Leu Thr Asp Tyr Leu Met Gly Ser
 210 215

<210> 57

<211> 237

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> (211)..(232)

<223> N = A, C, G OR T/U

<400> 57

ggatcccacc ttcaacacct tacaagtaaa gacaatgaag aacagttgaa acatgcaaaa 60

tatggagctt ttcattgtaat tactcttttta ctgtttacca ttcactataa ttcacaatta 120
aaattgtgtg actaaacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 180
aaaaaaaaaa aaaaaaaaaa aaaaaaaggg ngganaggnc gacncggccg cnaattc 237

<210> 58
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (2)..(8)
<223> XAA = ANYTHING

<400> 58
Glu Xaa Ala Ala Xaa Ser Xaa Xaa Pro Pro Phe Phe Phe Phe Phe Phe
1 5 10 15
Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
20 25 30
Phe Cys Leu Val Thr Gln Phe Leu Ile Ile Val Asn Gly Lys Gln Lys
35 40 45
Ser Asn Tyr Met Lys Ser Ser Ile Phe Cys Met Phe Gln Leu Phe Phe
50 55 60
Ile Val Phe Thr Cys Lys Val Leu Lys Val Gly Ser
65 70 75

<210> 59
<211> 199
<212> DNA
<213> Homo sapiens

<400> 59
ggatccctgg ctgccttctt catccgagga cgccgaggcc aagctcagca gcaccgcaca 60
cagcagcagc gtcagcccta tccggaccgc catcctcctc tcggggcccg tgccaacccc 120
tagagctgtc gccttcgcct ctgccaccac ggactcagcc accaccgccg cctcgccgcg 180
tcgacgcggc cgcgaattc 199

<210> 60
<211> 66
<212> PRT
<213> Homo sapiens

<400> 60
Asn Ser Arg Pro Arg Arg Arg Gly Glu Ala Ala Val Val Ala Glu Ser
1 5 10 15
Val Val Ala Glu Ala Lys Ala Thr Ala Leu Gly Val Gly Thr Gly Pro
20 25 30

Glu Arg Arg Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Cys Ala
 35 40 45

Val Leu Leu Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln
 50 55 60

Gly Ser
 65

<210> 61
 <211> 489
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (456) .. (489)
 <223> N = A, C, G OR T/U

<400> 61
 ggatccggca accatgacca gcgagaccac caccagggca ccaaagagga tcttggtgag 60
 gcagttcact tccaagtcga acaggccgat cttacttcgg ggatttgagg tattcatgac 120
 actccggagt tctctgccag tgtaaagaac aacacccaca acagtacctg atgcgaccac 180
 agtgccagcc cacagcgtgt tctctatgct caggctctcg ctgatcgggg ggtcgctgtc 240
 ttctcgggta aaagttccca cgaagttgtg aatgtcaata tttggctctt ctgcgtacac 300
 atacgatcga atctgaagaa ggtcggcggc cgtgggggagc ctctgcgtgc aggccacggg 360
 aagccgcagc ttccagtcgc tctccccatc cagctgatcc gtccgcaaga agcatgaccc 420
 gtttttttct gatgtcctca ggaagatcat gtcggnnggg acccgctggt cgangcggcc 480
 nccaattcn 489

<210> 62
 <211> 163
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1) .. (12)
 <223> XAA = ANYTHING

<400> 62
 Xaa Ile Gly Gly Arg Xaa Asp Gln Arg Val Pro Xaa Asp Met Ile Phe
 1 5 10 15

Leu Arg Thr Ser Glu Lys Asn Gly Ser Cys Phe Leu Arg Thr Asp Gln
 20 25 30

Leu Asp Gly Glu Thr Asp Trp Lys Leu Arg Leu Pro Val Ala Cys Thr
 35 40 45

Gln Arg Leu Pro Thr Ala Ala Asp Leu Leu Gln Ile Arg Ser Tyr Val
 50 55 60

Tyr Ala Glu Glu Pro Asn Ile Asp Ile His Asn Phe Val Gly Thr Phe
65 70 75 80

Thr Arg Glu Asp Ser Asp Pro Pro Ile Ser Glu Ser Leu Ser Ile Glu
85 90 95

Asn Thr Leu Trp Ala Gly Thr Val Val Ala Ser Gly Thr Val Val Gly
100 105 110

Val Val Leu Tyr Thr Gly Arg Glu Leu Arg Ser Val Met Asn Thr Ser
115 120 125

Asn Pro Arg Ser Lys Ile Gly Leu Phe Asp Leu Glu Val Asn Cys Leu
130 135 140

Thr Lys Ile Leu Phe Gly Ala Leu Val Val Val Ser Leu Val Met Val
145 150 155 160

Ala Gly Ser

<210> 63

<211> 392

<212> DNA

<213> Homo sapiens

<400> 63

ggatccgagt gctgatttgt acattgattc aggggagtaa ttggggagaa ggaaaaaggt 60
ggggtggaat gctggctcgg cctgccagt cacatgggtg gcagcagggc agctcagagg 120
ttgcctgaag agttcgtttt tcttgctcca gtccatctgc aggggcccgt ttgctgctgc 180
gtttctggtg ggccctctct ttggccatgg ccaggagat gttgaagtct aggatggggg 240
cggaggagga ggtagacgag ggcgctgtgg agtcctgttt tggggggctg tcttggnaat 300
tcagctcctc gctggtgtca ctggaggcgg atctcaccag ggctggcctg gggctctcca 360
aggetgectc tggtcgacgc ggccgcgaat tc 392

<210> 64

<211> 127

<212> PRT

<213> Homo sapiens

<400> 64

Ile Arg Gly Arg Val Asp Gln Arg Gln Pro Trp Arg Ala Pro Gly Gln
1 5 10 15

Pro Trp Asp Pro Pro Pro Val Thr Pro Ala Arg Ser Ile Xaa Lys Thr
20 25 30

Ala Pro Gln Asn Arg Thr Pro Gln Arg Pro Arg Leu Pro Pro Pro Pro
35 40 45

Thr Pro Ser Thr Ser Thr Ser Pro Trp Pro Trp Pro Lys Arg Gly Pro
50 55 60

Thr Arg Asn Ala Ala Ala Asn Gly Pro Leu Gln Met Asp Trp Ser Lys
 65 70 75 80

Lys Asn Glu Leu Phe Arg Gln Pro Leu Ser Cys Pro Ala Ala Thr His
 85 90 95

Val Thr Gly Arg Ala Glu Pro Ala Phe His Pro Thr Phe Phe Leu Leu
 100 105 110

Pro Asn Tyr Ser Pro Glu Ser Met Tyr Lys Ser Ala Leu Gly Ser
 115 120 125

<210> 65

<211> 577

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (551)..(575)

<223> N = A, C, G OR T/U

<400> 65

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ggatcctttc acaaaccag caaccatcac aaacagaagg acgagaatat taacagctgt 60
gaagacttta ttcacccaag cagactcttt tactccaaaa gacaaaagac ctgctagaag 120
taatataagg cacacagcaa aaaaatcggg atattctgca agaccagtgt aattcattct 180
gaagtatgtc ctcaaaaact gaccaatctg tttgctaaga agttcatcaa aggtgccact 240
ccaggtcttt gcaacacttg atgtacctat cacatacgat aaaatgagat tccagccagt 300
gatgaaggcc cacagctctc cgacagtcac gtaggtgtac aaatatgcag acccgtctt 360
gggaacacgg gcccacaaatt cggcatagca gaggccagcc atcactgaag ccagggcagc 420
aatgaggaag gacaccacga tgctggggcc cgagtctgcc ttggccacct cccagcgag 480
gacataaacc ccggcccca gggacttcc aacgccagg gcaatgaggt ccattggtgga 540
taagcagcgg nataatttgg ngnnntntan actgncc 577

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<210> 66

<211> 192

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (1)..(9)

<223> XAA = ANYTHING

<400> 66

Xaa Ser Xaa Xaa Xaa Xaa Lys Leu Xaa Arg Cys Leu Ser Thr Met Asp
 1 5 10 15

Leu Ile Ala Leu Gly Val Gly Ser Thr Leu Gly Ala Gly Val Tyr Val
 20 25 30

Leu Ala Gly Glu Val Ala Lys Ala Asp Ser Gly Pro Ser Ile Val Val

35

40

45

Ser Phe Leu Ile Ala Ala Leu Ala Ser Val Met Ala Gly Leu Cys Tyr
50 55 60

Ala Glu Phe Gly Ala Arg Val Pro Lys Thr Gly Ser Ala Tyr Leu Tyr
65 70 75 80

Thr Tyr Val Thr Val Gly Glu Leu Trp Ala Phe Ile Thr Gly Trp Asn
85 90 95

Leu Ile Leu Ser Tyr Val Ile Gly Thr Ser Ser Val Ala Arg Ala Trp
100 105 110

Ser Gly Thr Phe Asp Glu Leu Leu Ser Lys Gln Ile Gly Gln Phe Leu
115 120 125

Arg Thr Tyr Phe Arg Met Asn Tyr Thr Gly Leu Ala Glu Tyr Pro Asp
130 135 140

Phe Phe Ala Val Cys Leu Ile Leu Leu Leu Ala Gly Leu Leu Ser Phe
145 150 155 160

Gly Val Lys Glu Ser Ala Trp Val Asn Lys Val Phe Thr Ala Val Asn
165 170 175

Ile Leu Val Leu Leu Phe Val Met Val Ala Gly Phe Val Lys Gly Ser
180 185 190

<210> 67

<211> 719

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (500)..(714)

<223> N = A, C, G, OR T/U

<400> 67

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tggcttcac acatccacct tctccacccc aaaatggcac aaaagaaaca gttaccacac 120
cctgcagacc ttttggtgta aaagagatga tgatgaactg ggggtgggaac aggtcatgaa 180
gatctgtcta aaaaagtccc attcaggtga gttgtacac accatcaagc agcagacctc 240
tcatcaatta gggtaggga accaaggttc gattctcagg aaatcacaat ttcattcatt 300
tactcaatat gaatttaca agtgcctaca tattatccgc ttccacttgc agccatttct 360
agataaaaaa gaaacctggc atctcaaagg ggccaccaag ttctccccga gtctaccact 420
gaaaggacct tttttggaaa taggtttctt ctgtacctct ggaagggtaa catcttaaag 480
ctgaatcaac tttaacctgn agggctaaca tatttagcaa tacttgcatc ccagacatac 540
aacattaaaa gatacactaa attctgaagg tagctatgct gcaaaatagt tttaaaatta 600
aacaattgta cagtattcat ttatgcttgg aaattccagt cctagaccaa gcttgtggcc 660

accancattg accgttcttg ccatccagaa gagctgacag tgtcagttta atancctgg 719

<210> 68

<211> 227

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (2)..(67)

<223> XAA = ANYTHING

<400> 68

Arg Xaa Leu Asn His Cys Gln Leu Phe Trp Met Ala Arg Thr Val Asn
1 5 10 15

Xaa Gly Gly His Lys Leu Gly Leu Gly Leu Glu Phe Pro Ser Ile Asn
20 25 30

Glu Tyr Cys Thr Ile Val Phe Asn Tyr Phe Ala Ala Leu Pro Ser Glu
35 40 45

Phe Ser Val Ser Phe Asn Val Val Cys Leu Gly Cys Lys Tyr Cys Ile
50 55 60

Cys Pro Xaa Arg Leu Lys Leu Ile Gln Leu Asp Val Thr Leu Pro Glu
65 70 75 80

Val Gln Lys Lys Pro Ile Ser Lys Lys Gly Pro Phe Ser Gly Arg Leu
85 90 95

Gly Glu Asn Leu Val Ala Pro Leu Arg Cys Gln Val Ser Phe Leu Ser
100 105 110

Arg Asn Gly Cys Lys Trp Lys Arg Ile Ile Cys Arg His Phe Val Asn
115 120 125

Ser Tyr Val Asn Glu Asn Cys Asp Phe Leu Arg Ile Glu Pro Trp Phe
130 135 140

Pro Asn Pro Asn Glu Ala Arg Cys Leu Met Val Cys Thr Asn Ser Pro
145 150 155 160

Glu Trp Asp Phe Phe Arg Gln Ile Phe Met Thr Cys Ser His Pro Ser
165 170 175

Ser Ser Ser Ser Leu Leu His Gln Lys Val Cys Arg Val Trp Leu Phe
180 185 190

Leu Leu Cys His Phe Gly Val Glu Lys Val Asp Val Met Lys Pro Ile
195 200 205

Ile Gln Asp Leu Phe Leu Leu Val Leu Cys Phe Phe Phe Ala Leu Ala
210 215 220

Pro Gly Ser
225

<210> 69
<211> 311
<212> DNA
<213> Homo sapiens

<400> 69
ggatccgcgg tacgcccgcc cgtgctcgcg cgtcagcgcg gcgatgtcct cgcgcacatctc 60
gttgatgacc gggagcagaa actgctcgaa atcctcctcg gggtccagca cctccacttc 120
ctccgggtcc gccagctcga cgatgtccag gggccgcacg tcttcccact gcctcggaac 180
cgcaatagcg atgtctgttg gagagagaaa accgacactc gctatgctta gcaatagaga 240
gcccgaaat tcttgaaaac ttttaccctt tttcaacttt tcttctcaga ggtcgcgcgcg 300
gccgcgaatt c 311

<210> 70
<211> 102
<212> PRT
<213> Homo sapiens

<400> 70
Ile Arg Gly Arg Val Asp Leu Glu Glu Lys Leu Lys Lys Gly Lys Ser
1 5 10 15
Phe Gln Glu Tyr Ser Gly Ser Leu Leu Leu Ser Ile Ala Ser Val Gly
20 25 30
Phe Leu Ser Pro Thr Asp Ile Ala Ile Ala Val Pro Arg Gln Trp Glu
35 40 45
Glu Met Arg Pro Leu Asp Ile Val Glu Leu Ala Glu Pro Glu Glu Val
50 55 60
Glu Val Leu Glu Pro Glu Glu Asp Phe Glu Gln Phe Leu Leu Pro Val
65 70 75 80
Ile Asn Glu Met Arg Glu Asp Ile Ala Ser Leu Thr Arg Glu His Gly
85 90 95
Arg Ala Tyr Arg Gly Ser
100

<210> 71
<211> 501
<212> DNA
<213> Homo sapiens

<400> 71
ggatccggtg ctgccaatta aaaaaaaaaac tgtaaactcat cttaccaccc aaaagtgata 60
tggaactgtg tttgaatctg agcatggaca tggtttagt catcttttgg aattataagt 120


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gaaagtgata ggtaactcct tgtgttccat ttctcagagt agattgctat atccaaatga 180
tcatgaacac ccctcccatc ccacactcag atggaaagca gccagaaccc ctgccactgg 240
attcttcagc acccttggga cagtctccaa ctgacacttc ccagcagggg aggagggcag 300
gcacctttgg tgactcttca gtgagactcc atcgacattc agaatcttaa aatgttggtg 360
atgaaaacca tggacctcca agtcactcctt accaacctta aatgtagtgt tgtgacatcc 420
aacgaaggac ttccacgtca cgtgggaata aatttgaaca gatacatcca attgaacata 480
ggtcgacgcg gccgcgaatt c
501

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<210> 72
<211> 163
<212> PRT
<213> Homo sapiens

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<400> 72
Glu Phe Ala Ala Ala Ser Thr Tyr Val Gln Leu Asp Val Ser Val Gln
 1             5             10             15
Ile Tyr Ser His Val Thr Trp Lys Ser Phe Val Gly Cys His Asn Thr
          20             25             30
Thr Phe Lys Val Gly Lys Asp Asp Leu Glu Val His Gly Phe His Tyr
          35             40             45
Gln His Phe Lys Ile Leu Asn Val Asp Gly Val Ser Leu Lys Ser His
          50             55             60
Gln Arg Cys Leu Pro Ser Ser Pro Ala Gly Lys Cys Gln Leu Glu Thr
          65             70             75             80
Val Pro Arg Val Leu Lys Asn Pro Val Ala Gly Val Leu Ala Ala Phe
          85             90             95
His Leu Ser Val Gly Trp Glu Gly Cys Ser Ser Phe Gly Tyr Ser Asn
          100            105            110
Leu Leu Glu Met Glu His Lys Glu Leu Pro Ile Thr Phe Thr Tyr Asn
          115            120            125
Ser Lys Arg Leu Gln Pro Cys Pro Cys Ser Asp Ser Asn Ser Phe Pro
          130            135            140
Tyr His Phe Trp Val Val Arg Phe Thr Val Phe Phe Leu Ile Gly Ser
          145            150            155            160
Thr Gly Ser

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<210> 73
<211> 747
<212> DNA
<213> Homo sapiens

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<400> 73

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ggatcctgtt gcttcaaaag tcaattttat agaatcccaa ggtgtctgtt ctttggatat 60
 gagtcggaaa tgaggaggat ttcttggaga aacttctggg gcaggaagat accagttttt 120
 cctgatcaga aagtgcacnt ggaagatacc aaggaaaacc acaaagaggt gcattctcct 180
 cacagtgagc tcggatacta tcattgatct caggaatgtg aggggttatg tgagaaattc 240
 cagtataatc aaaccattg atccatattc cagagtcccg ttttaactgca tttccttcca 300
 agtcatggaa tgttctagtc atatgctgaa gaaacactct ctttggcttc ggattagcag 360
 gattggagct atatggaaaa aatgttccac tgcaaacaag gaggaatgta attgcacata 420
 ccaaagttaa agttagcatg gttttttttg tgctcttggc aaggtagatg aagttaatca 480
 tgtaataaaa tcttttcgca agagtatgta taagtattat tttggctaca gttgcagttc 540
 catcacagaca aacggagacc atagaagtgg ttataccatg agagagactg tccaataaga 600
 gagatgaaca ctgctataat gagaacggta acaaggctag tgaaccagct gatcaaagtg 660
 atgccaagtc cacacaagaa gtccttcttg tagttaccag tcttatgttt gggctgcaaa 720
 aattttttgc ccaggtagaa aacaaca 747

<210> 74

<211> 238

<212> PRT

<213> Homo sapiens

<400> 74

Cys Cys Phe Val Pro Gly Gln Lys Ile Phe Ala Ala Gln Thr Asp Trp
 1 5 10 15
 Leu Gln Glu Gly Leu Leu Val Trp Thr Trp His His Phe Asp Gln Leu
 20 25 30
 Val His Pro Cys Tyr Arg Ser His Tyr Ser Ser Val His Leu Ser Tyr
 35 40 45
 Trp Thr Val Ser Leu Met Val Pro Leu Leu Trp Ser Pro Phe Val Cys
 50 55 60
 Met Glu Leu Gln Leu Pro Lys Tyr Leu Tyr Ile Leu Leu Arg Lys Asp
 65 70 75 80
 Phe Ile Thr Leu Thr Ser Ser Thr Leu Pro Arg Ala Gln Lys Lys Pro
 85 90 95
 Cys Leu Leu Trp Tyr Val Gln Leu His Ser Ser Leu Phe Ala Val Glu
 100 105 110
 His Phe Phe His Ile Ala Pro Ile Leu Leu Ile Arg Ser Gln Arg Glu
 115 120 125
 Cys Phe Phe Ser Ile Leu Glu His Ser Met Thr Trp Lys Glu Met Gln
 130 135 140
 Leu Asn Gly Thr Leu Glu Tyr Gly Ser Met Gly Leu Ile Ile Leu Glu
 145 150 155 160
 Phe Leu Thr Pro Leu Thr Phe Leu Arg Ser Met Ile Val Ser Glu Leu
 165 170 175
 Thr Val Arg Arg Met His Leu Phe Val Val Phe Leu Gly Ile Phe Xaa

180

185

190

Val His Phe Leu Ile Arg Lys Asn Trp Tyr Leu Pro Ala Pro Glu Val
 195 200 205

Ser Pro Arg Asn Pro Pro His Phe Arg Leu Ile Ser Lys Glu Gln Thr
 210 215 220

Pro Trp Asp Ser Ile Lys Leu Thr Phe Glu Ala Thr Gly Ser
 225 230 235

<210> 75

<211> 712

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (712)

<223> N = A, C G OR T/U

<400> 75

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 tctactatgt atacagcagt cttgaataaa ctgcaaacat gtaacaacag ttataatttg 120
 aaagagtctt ccaaagtga acattctggc ctagaaccct tcccatctcc atcaaccag 180
 aagacatcaa attttcagaa gacaatcttt cctaggactt gtaaaacaaa atgtacaaaa 240
 tatattagtt tactaactct acttttgtca taaactggca acctctttaa catccagaaa 300
 gactagatgt tgtcaattag gactcgtctg tcctttatgt acactatata cacagataag 360
 taaaacaaaa tgcacagaca taatgattca tcttgccctg ctgtaaacag gatggcatag 420
 agctctctgc acctccccct cctctctcct cccctgaacc actgcacaaa cacaatgagt 480
 attactcaac aggtgatttg gccattcccc cccaaaaata tttcctatga attgtaacaa 540
 aaaggatttt acaaaatgtg attttgctac ctctaatttt aacatatcag gcacttcaga 600
 acatctaaaa agaagagaca tttcaaaaaa gcttagcatt gtcaactata tacacagtag 660
 tgaggaataa aatgcacaca aaacaatgga tagaatatga aaatgtcttc tn 712

<210> 76

<211> 227

<212> PRT

<213> Homo sapiens

<400> 76

Arg Arg His Phe His Ile Leu Ser Ile Val Leu Cys Ala Phe Tyr Ser
 1 5 10 15

Ser Leu Leu Cys Ile Leu Thr Met Leu Ser Phe Phe Glu Met Ser Leu
 20 25 30

Leu Phe Arg Cys Ser Glu Val Pro Asp Met Leu Lys Leu Glu Val Ala
 35 40 45

Lys Ser His Phe Val Asn Thr Phe Leu Leu Gln Phe Ile Gly Asn Ile
 50 55 60

Phe Gly Gly Glu Trp Pro Asn His Leu Leu Ser Asn Thr His Cys Val
65 70 75 80

Cys Ala Val Val Gln Gly Arg Arg Glu Glu Gly Glu Val Gln Arg Ala
85 90 95

Leu Cys His Pro Val Tyr Ser Glu Ala Arg Ile Ile Met Ser Val His
100 105 110

Phe Val Leu Leu Ile Cys Val Tyr Ser Val His Lys Gly Gln Thr Ser
115 120 125

Pro Asn Gln His Leu Val Phe Leu Asp Val Lys Glu Val Ala Ser Val
130 135 140

Gln Lys Ser Thr Asn Ile Phe Cys Thr Phe Cys Phe Thr Ser Pro Arg
145 150 155 160

Lys Asp Cys Leu Leu Lys Ile Cys Leu Leu Gly Trp Arg Trp Glu Gly
165 170 175

Phe Ala Arg Met Phe Thr Phe Gly Arg Leu Phe Gln Ile Ile Thr Val
180 185 190

Val Thr Cys Leu Gln Phe Ile Gln Asp Cys Cys Ile His Ser Arg Gln
195 200 205

Ile Asn Ser Leu Leu Glu Thr Ser Ser Leu Ser Arg Cys Leu Glu Val
210 215 220

Pro Gly Ser
225

<210> 77
<211> 605
<212> DNA
<213> Homo sapiens

<400> 77
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gatggcagat acacttctta caagtccagc aaaatacact aagtttttca tgggtgatttt 120
cacatttgct cttttcattt tcttcatgtt tgggtgagact gcagagttga agagtatcaa 180
gctgttggtg tactttcttct gcccaacgac aatttactag ttctcgtagc tggagtggag 240
cacggcaatg aggacattga gctctctgct ctgtcagcca gcgcctaata cagctgaaac 300
aacacagttt ggagcaatga ggacacaggc gtgcatcccg caatttctcc atacaaatga 360
aacatcgga aacctcagca atgctctcca cgctctgttc atccattgcc tccggtctc 420
ggcgggggccg ctggcgaccc gcaggctccg cagtctgacc tcttaggcgc cggcccagg 480
tcgccagatc aaatcgccga taaaagccc gcgcccacgt cagggggctc tgacaaccgc 540
cccacctgcg cgccccatct cttcagggtcc agcgccgcct accccgtcga cgcggccgcg 600
aatte 605

<210> 78
<211> 195

<212> PRT
<213> Homo sapiens

<400> 78

Ile Arg Gly Arg Val Asp Gly Val Gly Gly Ala Gly Pro Glu Glu Met
1 5 10 15

Gly Arg Ala Gly Gly Ala Val Val Arg Ala Pro Arg Gly Arg Arg Ala
20 25 30

Phe Ile Gly Asp Leu Ile Trp Arg Pro Arg Ala Gly Ala Glu Val Arg
35 40 45

Leu Arg Ser Leu Arg Val Ala Ser Gly Pro Ala Glu Ser Arg Arg Gln
50 55 60

Trp Met Asn Arg Ala Trp Arg Ala Leu Leu Arg Phe Ser Asp Val Ser
65 70 75 80

Phe Val Trp Arg Asn Cys Gly Met His Ala Cys Val Leu Ile Ala Pro
85 90 95

Asn Cys Val Val Ser Ala Val Leu Gly Ala Gly Gln Ser Arg Glu Leu
100 105 110

Asn Val Leu Ile Ala Val Leu His Ser Ser Tyr Glu Asn Ile Val Val
115 120 125

Gly Gln Lys Lys His Asn Ser Leu Ile Leu Phe Asn Ser Ala Val Ser
130 135 140

Pro Asn Met Lys Lys Met Lys Arg Thr Asn Val Lys Ile Thr Met Lys
145 150 155 160

Asn Leu Val Tyr Phe Ala Gly Leu Val Arg Ser Val Ser Ala Ile Ser
165 170 175

Val His Phe Gly Glu Glu Cys Met Ala Asp Ile Pro Leu Asn Leu Trp
180 185 190

Gln Gly Ser
195

<210> 79
<211> 875
<212> DNA
<213> Homo sapiens

<220>

<221> modified_base

<222> (569)..(875)

<223> N = A, C, G OR T/U

<400> 79

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ggatccatta cctttgaaag agccaaaaaa caaaaaaaaaa aaaaaaaaaa aattaccatg 60
ccagttttat tcccgttgaa tatttacacc ttggacagca aaccttgctc acataaagta 120
gaaaacagat acaataaaac atggcttgaa aaatgaccag agtatgcacc tgtagtactg 180
tactactaaat aaaatacaca aggcagcaat acttaggggc cagaaacact gcttactaca 240
agtcagttac ggaatcataa tttacagtaa aaatggggc gtcccaaggc tcaatttttc 300
tttttctttt gtcatttaca gtagaataaa tattttgttg ctattgctac actttaattt 360
acattctaac ctattaaatg cagaaagcta gtgtaaagca tatagattaa gtgtagggtcc 420
catacgtatg acagtttggt caagactagt aggtttttgt ttttgtatct ttttttaact 480
tattaaatgg ctagtgggaa agatttgtgc ttgtgatcag ctcttaactt caattttaca 540
tcaaaacgtc cctgaaaacg gtctttctna ctggacccaa tgttctcacc gtacgcctta 600
cactntatgc gaattcagtg tccatggtaa gatgggtgaa tgtacggccg caaggggctt 660
naagtanttg gcttgaagga attgcctagt ccggaaatct gcaaggaaac caggggagtt 720
gccagtccaa atctcccatt ccacttatct tacttattnn ttgccgtgac tgacggaagg 780
ctttgggtna cttatcntgg gaagntccag gctattttgg agctagtga nctaactggt 840
gnctttaaaa gccggttgcc tttgaccaa attan 875

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<210> 80
<211> 276
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (11)..(65)
<223> XAA = ANYTHING

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<400> 80
Asn Phe Gly Gln Arg Gln Pro Ala Phe Lys Xaa Thr Ser Xaa Asn Leu
 1             5             10             15
Gln Asn Ser Leu Xaa Leu Pro Xaa Ile Ser Xaa Pro Lys Pro Ser Val
          20             25             30
Ser His Gly Xaa Xaa Val Arg Val Glu Trp Glu Ile Trp Thr Gly Asn
          35             40             45
Ser Pro Gly Phe Leu Ala Asp Phe Arg Thr Arg Gln Phe Leu Gln Ala
          50             55             60
Xaa Tyr Xaa Lys Pro Leu Ala Ala Val His Ser Pro Ile Leu Pro Trp
          65             70             75             80
Thr Leu Asn Ser His Xaa Val Gly Val Arg Glu His Trp Val Gln Xaa
          85             90             95
Glu Arg Pro Phe Ser Gly Thr Phe Cys Lys Ile Glu Val Lys Ser Ser
          100            105            110
Gln Ala Gln Ile Phe Pro Thr Ser His Leu Ile Ser Lys Lys Ile Gln
          115            120            125
Lys Gln Lys Pro Thr Ser Leu Glu Gln Thr Val Ile Arg Met Gly Pro
          130            135            140

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Thr Leu Asn Leu Tyr Ala Leu His Leu Ser Ala Phe Asn Arg Leu Glu
145 150 155 160

Cys Lys Leu Lys Cys Ser Asn Ser Asn Lys Ile Phe Ile Leu Leu Met
165 170 175

Thr Lys Glu Lys Glu Lys Leu Ser Leu Gly Thr Cys Pro Phe Leu Leu
180 185 190

Ile Met Ile Pro Leu Thr Cys Ser Lys Gln Cys Phe Trp Pro Leu Ser
195 200 205

Ile Ala Ala Leu Cys Ile Leu Phe Ser Val Gln Tyr Tyr Arg Cys Ile
210 215 220

Leu Trp Ser Phe Phe Lys Pro Cys Phe Ile Val Ser Val Phe Tyr Phe
225 230 235 240

Met Ala Arg Phe Ala Val Gln Gly Val Asn Ile Gln Arg Glu Asn Trp
245 250 255

His Gly Asn Phe Phe Phe Phe Phe Phe Leu Phe Phe Gly Ser Phe Lys
260 265 270

Gly Asn Gly Ser
275

<210> 81
<211> 631
<212> DNA
<213> Homo sapiens

<400> 81
ggatccctcc acctcgatct tgccgcagtc tgcgatgata acatccttca ggggtttatc 60
ccggctgtct gtcttggtgc tctccacctt ccgcaccacc tccatgccct ctagaacttt 120
gccaaacacc acatgcttgc catctagcca ggctgtcttg actgtcgtga tgaagaactg 180
ggagccggtt gtgtctttgc ctgcgttggc catgctcacc cagccaggcc cgtagtgttt 240
cagtttgaag ttctcatcgg ggaagcgctc accgtagatg ctctttcctc ctgtgccatc 300
tcccctgggt aagtctccgc cctggatcat gaagtccttg attacacgat ggaatttgct 360
gtttttgtag ccaaattcct tctctcctgt agctaaggcc acaaaattat ccactgtttt 420
tggaacagtc tttccgaaga gaccaaagat caccgcgcct acatcttcat ctccaattcg 480
taggtcaaaa tacaccttga cggtgacttt gggccccttc ttctttctcat cgccgcgaga 540
aggtcccggc agcagcagga agaagacgga ccccgcgatg aaggcggcgg caaggagcac 600
ccttatgttg cgtcgacgcg gccgcgaatt c 631

<210> 82
<211> 210
<212> PRT
<213> Homo sapiens

<400> 82
Asn Ser Arg Pro Arg Arg Arg Asn Ile Arg Val Leu Leu Ala Ala Ala
1 5 10 15

Phe Ile Ala Gly Ser Val Phe Phe Leu Leu Leu Pro Gly Pro Ser Ala
 20 25 30
 Ala Asp Glu Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe
 35 40 45
 Asp Leu Arg Ile Gly Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu
 50 55 60
 Phe Gly Lys Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala
 65 70 75 80
 Thr Gly Glu Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val
 85 90 95
 Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
 100 105 110
 Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
 115 120 125
 Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
 130 135 140
 Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala
 145 150 155 160
 Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
 165 170 175
 Glu Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
 180 185 190
 Pro Leu Lys Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu
 195 200 205
 Gly Ser
 210

<210> 83
 <211> 452
 <212> DNA
 <213> Homo sapiens

<400> 83
 ggatccgccc attgtaattc catgaataag tgcaacataa ggtttctggc aagaacctga 60
 aagaaacaga gcaacagcat tattcagcat atattcttct ctgaagaaaa ctggagctat 120
 cttctgtttt gccttttcag cttccgagat cactaggaag gaaagattac aaataaaaaa 180
 aaaaagattt aatagtcaac attgtcaact agatcaaaag tattatgaaa attaaatact 240
 gggggaaggg agtactctaa aatgacttgt taaaagtgtt gaagttgccc ctgccacaga 300
 cattatatta tagtcacaga tccatagtc aatgtcaaag cttcaaggca aaaattccta 360
 ttcttggttt ccatgcttct tacaaaatgt tagattagaa attataggct gggcatggtg 420
 gctcaaacct gtgtcgacgc ggccgcgaat tc 452

<210> 84
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 84
 Ile Arg Gly Arg Val Asp Thr Gly Leu Ser His His Ala Gln Pro Ile
 1 5 10 15
 Ile Ser Asn Leu Thr Phe Cys Lys Lys His Gly Lys Gln Glu Glu Phe
 20 25 30
 Leu Pro Ser Phe Asp Ile Gly Leu Trp Ile Cys Asp Tyr Asn Ile Met
 35 40 45
 Ser Val Ala Gly Ala Thr Ser Lys Leu Leu Thr Ser His Phe Arg Val
 50 55 60
 Leu Pro Ser Pro Ser Ile Phe Ser Tyr Phe Ser Ser Gln Cys Leu Leu
 65 70 75 80
 Asn Leu Phe Phe Phe Ile Cys Asn Leu Ser Phe Leu Val Ile Ser Glu
 85 90 95
 Ala Glu Lys Ala Lys Gln Lys Ile Ala Pro Val Phe Phe Arg Glu Glu
 100 105 110
 Tyr Met Leu Asn Asn Ala Val Ala Leu Phe Leu Ser Gly Ser Cys Gln
 115 120 125
 Lys Pro Tyr Val Ala Leu Ile His Gly Ile Thr Met Gly Gly Ser
 130 135 140

<210> 85
 <211> 752
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (462)..(748)
 <223> N = A, C, G OR T/U

<400> 85
 ggatccggtc aggggaaaga agggccggtc ctggatctgg cagtaccaga gcagcagcaa 60
 cagcaggagc agcaggggca gcagcaggct gccgatttcc agcccggagg ggccgggctc 120
 ggaccccggc gggcaggggg gatttggggg accgactctc gtggacacgt ggcagtggag 180
 aacgcagttg ggaggaggt gaaggctgcc cagggtctgg gtgtcgtcgc ctagcagctg 240
 cccttggtag atgagtcgca cctgctgttc ccggccggga aactgggtcc ttttcaagga 300
 gccaatggtg tcgtggggcc aggcctggc cacctgctct gaatcattga ggaatttcag 360
 cccgtagcac gaggggctcc tgcggggagt ccggggctgg cgggtgttgc gtgaaccccg 420
 tgctgggctc tggctgtgca gcttgacctt ctggtgtctc angtggggg tctctgcccc 480

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tggggccttc cctctcatgc tgtcggtagc tgccatggct tgccgctggg ctgggatggc 540
gttgggggtcc ctgacggtcg gggcaatggg tccccggcct tnacggtgtg ccttgaaaac 600
ccagccangg ccaacaccag aanggcaagg caagcnccga naaaaggacg gtcacttcat 660
cacccaaccc nttnatcang gtcattngcg ctggcttgcc cgccggcnta ccgancgccg 720
ggttcccccان ttccttnacc cgcccggnaa tt 752

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<210> 86
<211> 247
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (1)..(94)
<223> XAA = ANYTHING

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<400> 86
Xaa Pro Ala Gly Xaa Arg Xaa Trp Gly Thr Arg Arg Ser Val Xaa Arg
  1              5              10              15

Arg Ala Ser Gln Ala Xaa Pro Xaa Xaa Gly Trp Val Met Lys Pro Ser
      20              25              30

Phe Xaa Arg Xaa Leu Pro Cys Xaa Ser Gly Val Gly Xaa Gly Trp Val
      35              40              45

Phe Lys Ala His Arg Xaa Gly Arg Gly Pro Ile Ala Pro Ala Val Arg
      50              55              60

Asp Pro Asn Ala Ile Pro Ala Gln Arg Gln Ala Met Ala Ala Thr Asp
      65              70              75              80

Ser Met Arg Gly Lys Ala Pro Gly Ala Glu Thr Pro Ser Xaa Arg His
      85              90              95

Gln Lys Val Lys Leu His Ser Gln Ser Pro Ala Arg Gly Ser Gln Gln
      100              105              110

His Arg Gln Pro Arg Thr Pro Arg Arg Ser Pro Ser Cys Tyr Gly Leu
      115              120              125

Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp Pro His Asp
      130              135              140

Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly Arg Glu Gln Gln
      145              150              155              160

Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly Asp Asp Thr Gln Thr
      165              170              175

Leu Gly Ser Leu His Leu Pro Pro Asn Cys Val Leu His Cys His Val
      180              185              190

Ser Thr Arg Val Gly Pro Pro Asn Pro Pro Cys Pro Pro Gly Ser Glu

```

195

200

205

Pro Gly Pro Ser Gly Leu Glu Ile Gly Ser Leu Leu Leu Pro Leu Leu
 210 215 220

Leu Leu Leu Leu Leu Leu Leu Trp Tyr Cys Gln Ile Gln Tyr Arg Pro
 225 230 235 240

Phe Phe Pro Leu Thr Gly Ser
 245

<210> 87

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (375)..(395)

<223> N = A, C, G OR T/U

<400> 87

ggatccaga gtattctgac agataaaatc ggggaggcag ttatgaatac cactctcaca 60
 ctcgtaata tctttgcagc tattgtcctc tgtgagctca tagccagtc cgcagctgct 120
 gtcccgctgg cagcggaaag agccactgt gttgatgcag gattctccaa gccggcagct 180
 gtggctgccc gtgatgcatt cattgacatc ttcacaggag acaccatcag acagcagctg 240
 gtagccacg aagcaggagc agaccacctc gtcacccgtg tctcggcact gctgcttgca 300
 gggcccgcc cctcggcagc ggtcattcag atatgggtcc tcttgcttcc cctcaacctc 360
 aatgatctta tccgnnnttg gangccccc acntnc 396

<210> 88

<211> 132

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (1)..(8)

<223> XAA = ANYTHING

<400> 88

Xaa Xaa Xaa Gly Xaa Pro Xaa Xaa Asp Lys Ile Ile Glu Val Glu Glu
 1 5 10 15

Glu Gln Glu Asp Pro Tyr Leu Asn Asp Arg Cys Arg Gly Gly Gly Pro
 20 25 30

Cys Lys Gln Gln Cys Arg Asp Thr Gly Asp Glu Val Val Cys Ser Cys
 35 40 45

Phe Val Gly Tyr Gln Leu Leu Ser Asp Gly Val Ser Cys Glu Asp Val
 50 55 60

Asn Glu Cys Ile Thr Gly Ser His Ser Cys Arg Leu Gly Glu Ser Cys
 65 70 75 80

Ile Asn Thr Val Gly Ser Phe Arg Cys Gln Arg Asp Ser Ser Cys Gly
 85 90 95

Thr Gly Tyr Glu Leu Thr Glu Asp Asn Ser Cys Lys Asp Ile Asp Glu
 100 105 110

Cys Glu Ser Gly Ile His Asn Cys Leu Pro Asp Phe Ile Cys Gln Asn
 115 120 125

Thr Leu Gly Ser
 130

<210> 89
 <211> 558
 <212> DNA
 <213> Homo sapiens

<400> 89
 ggatccagac ccacgagggg catatgaatt ttcattcagc agcttgatgg tgctgggtgaa 60
 gtctgtgctg tccagtttct cgcacaactt tctcttcagg tcatcccaat ataagcgacg 120
 tgctgcaggg aagtcctctc ctggctcctc cctcactgga gactcggttc ctgccagtct 180
 ctcacactca gtttttggtt ctaccccttt acaatagccc aagtagccaa tcataaatcc 240
 aatcaagaaa aagacgatca cagcaatagt cccatagcag atacttccac tacacctttt 300
 tggntttgtg acattggcct ttgtgttatt gtcagcattt tcttcttcat ctacagcaag 360
 tttcatctnc acatgactgt tatcgccatc tacttgccga gccaggetga accgggtata 420
 tgacaatggt tctccaccaa acaagttaga gaatgctgat ctagcttgat ccatcattct 480
 gaactgccac acagaagaca ctagcgcgtc ctncgtcccg agccgcaccc gatatcccgt 540
 cgacgcggcc gcgaattc 558

<210> 90
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (16)..(85)
 <223> XAA = ANYTHING

<400> 90
 Glu Phe Ala Ala Ala Ser Thr Gly Tyr Arg Val Arg Leu Gly Thr Xaa
 1 5 10 15

Asp Ala Leu Val Ser Ser Val Trp Gln Phe Arg Met Met Asp Gln Ala
 20 25 30

Arg Ser Ala Phe Ser Asn Leu Phe Gly Gly Glu Pro Leu Ser Tyr Thr
 35 40 45

Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp Asn Ser His Val Xaa

50 55 60
 Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala Asp Asn Asn Thr Lys
 65 70 75 80
 Ala Asn Val Thr Xaa Pro Lys Arg Cys Ser Gly Ser Ile Cys Tyr Gly
 85 90 95
 Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly Phe Met Ile Gly Tyr
 100 105 110
 Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu
 115 120 125
 Ala Gly Thr Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro
 130 135 140
 Ala Ala Arg Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu
 145 150 155 160
 Lys Leu Asp Ser Thr Asp Phe Thr Ser Thr Ile Lys Leu Leu Asn Glu
 165 170 175
 Asn Ser Tyr Val Pro Arg Gly Ser Gly Ser
 180 185

<210> 91
 <211> 461
 <212> DNA
 <213> Homo sapiens

<400> 91
 ggatcccttt gtatataaaa tgggtgaaagc tgacttgaat gtgccgtcac cactctgctg 60
 ggaaaaacag atgaaggtgg cccagagaaa accacagact ccagcgtaag ctgttctcca 120
 ttgaacagga acaaggctga agttgggtcag ctgtacaaag ggccagtaca tcagtccact 180
 cagataggta ttccagaatt tctgtttcag gtccaaaaat atgtcatcct ttccttggag 240
 aatgctcata ccgacataga aggccgagac cgcgatgggc gcaccgacca cctgggtcgca 300
 cagcaacttg gccagcaggg cgtgcggcgc tcggcccggg agcgcgcgct ccagcaggcg 360
 cagccacacg tagttgaagt tggcgtggaa ggtcaccacc aacgtggcca cgcgccgcgt 420
 ctggcgccag ttggcctcgc ggtcgacgcg gccgcgaatt c 461

<210> 92
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 92
 Ile Arg Gly Arg Val Asp Arg Glu Ala Asn Trp Arg Gln Thr Arg Arg
 1 5 10 15
 Val Ala Thr Leu Val Val Thr Phe His Ala Asn Phe Asn Tyr Val Trp
 20 25 30

Leu Arg Leu Leu Glu Arg Ala Leu Pro Gly Arg Ala Pro His Ala Leu
 35 40 45

Leu Ala Lys Leu Leu Cys Asp Gln Val Val Gly Ala Pro Ile Ala Val
 50 55 60

Ser Ala Phe Tyr Val Gly Met Ser Ile Leu Gln Gly Lys Asp Asp Ile
 65 70 75 80

Phe Leu Asp Leu Lys Gln Lys Phe Trp Asn Thr Tyr Leu Ser Gly Leu
 85 90 95

Met Tyr Trp Pro Phe Val Gln Leu Thr Asn Phe Ser Leu Val Pro Val
 100 105 110

Gln Trp Arg Thr Ala Tyr Ala Gly Val Cys Gly Phe Leu Trp Ala Thr
 115 120 125

Phe Ile Cys Phe Ser Gln Gln Ser Gly Asp Gly Thr Phe Lys Ser Ala
 130 135 140

Phe Thr Ile Leu Tyr Thr Lys Gly Ser
 145 150

<210> 93

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (541)..(567)

<223> N = A, C, G OR T/U

<400> 93

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ggatccagtg ctataataac nattacacac attgtaactc ctacacaatt tgaaattttc 60
aagttaagac aaaggtaact atatatagaa gcagtatggt ttctgaaccc ttacagattg 120
ttttgcacac tcctggatta cacacatctc atcaatctca agaataaaat caaagtcttt 180
ggcttgacag ctttcacaa tctgacctct gttttctcgc cagcctcatc tcctgtcatt 240
cacaacattt ccagcattcc aaccagtctg aacttttgca gtttcccacg tgcgctaggc 300
tctttcttca tcagcatctc tatgcatgct gtctcctgct actggaatgc cctcattctc 360
gttgcttcct gttttgaaga aaagctgtga taccggcaac agtggtttaag tatcacacgg 420
gtagttaaaa ggcaagttgg tcctatctga catgtggaaa tggccagctc gttagaaggc 480
agtacctggt gaagcccggg cagcgcaggt cagccagcg acagtggaaa gcccttcctt 540
ngcaagcgcg cttccggcac tagccgnacc ccgncgagct ctggtcgacg cggccgcgaa 600
ttc
603

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<210> 94

<211> 195

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (13)

<223> XAA = ANYTHING

<400> 94

Glu Phe Ala Ala Ala Ser Thr Arg Ala Arg Arg Gly Xaa Ala Ser Ala
1 5 10 15

Gly Ser Ala Leu Ala Arg Glu Gly Leu Ser Thr Val Ala Gly Val Asn
20 25 30

Ser Arg Ala Arg Ala Ser Pro Gly Thr Ala Phe Arg Ala Gly His Phe
35 40 45

His Met Ser Asp Arg Thr Asn Leu Pro Phe Asn Tyr Pro Cys Asp Thr
50 55 60

Thr Leu Leu Pro Val Ser Gln Leu Phe Phe Lys Thr Gly Ser Asn Glu
65 70 75 80

Asn Glu Gly Ile Pro Val Ala Gly Asp Ser Met His Arg Asp Ala Asp
85 90 95

Glu Glu Arg Ala Arg Thr Trp Glu Thr Ala Lys Val Gln Thr Gly Trp
100 105 110

Asn Ala Gly Asn Val Val Asn Asp Arg Arg Gly Trp Arg Glu Asn Arg
115 120 125

Gly Gln Ile Val Glu Gly Cys Gln Ala Lys Asp Phe Asp Phe Ile Leu
130 135 140

Glu Ile Asp Glu Met Cys Val Ile Gln Glu Cys Ala Lys Gln Ser Val
145 150 155 160

Arg Val Gln Lys Thr Tyr Cys Phe Tyr Ile Leu Pro Leu Ser Leu Glu
165 170 175

Asn Phe Lys Leu Cys Arg Ser Tyr Asn Val Cys Asn Xaa Tyr Tyr Ser
180 185 190

Thr Gly Ser
195

<210> 95

<211> 813

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (529)..(779)

<223> N = A, C, G OR T/U

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<400> 95
ggatcctact gaaatggaaa aggttgaaaa atgtatcagt gatgccatga gttggctgaa 60
tagtaagatg aatgcacaga acaaactaag tctcactcaa gatcctgtgg taaaagtttc 120
agaaatagta gcaaagtcaa aggaactgga taatttctgt aaccccatca tttacaagcc 180
caaaccaaaa gcagaagttc ctgaagacaa accaaaagct aatagtgaac acaatggccc 240
aatggatgga cagagtggaa ctgaaactaa atcagattca aaaaagaca gctcacagca 300
tactaaatcc tctggagaga tggaagtgga ctaagtctta attttacctt cacattaatt 360
caaaccgtgc aagtaaccac ggggtccatc ttttacatct ggtacacaca acagacgctc 420
agttgttctt aaccactttt gtcatttggg ttttggagta gttttgaaaa gtggtttata 480
ttgagtgcac ttctggatcat ttccattgct gcttatatgc agtggtagnc cgaattagat 540
ttaccaggac aatctaagct ttccggataa ttttatatat caaacattcn ggatggatac 600
ctagttggca acagtctacc ttatttaagc ttctactggg ataaacctca ttncctttatt 660
caggaaagga tctttaatgn antattggtg naaaagccta gattaatngc tcttantttg 720
aaaaccaatg gaaaattgga ngggnttaaa gttccgaggc ctggcctttt ttagtatggg 780
atgntccant taaataaact caattttcct ctt                                     813

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<210> 96
<211> 258
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (8)..(70)
<223> XAA = ANYTHING

```

```

<400> 96
Lys Arg Lys Ile Glu Phe Ile Xaa Xaa His Pro Ile Leu Lys Lys Ala
 1               5               10               15

Arg Pro Arg Asn Phe Xaa Pro Xaa Gln Phe Ser Ile Gly Phe Gln Xaa
          20               25               30

Lys Ser Xaa Ser Arg Leu Xaa His Gln Xaa Xaa Ile Lys Asp Pro Phe
          35               40               45

Leu Asn Lys Xaa Met Arg Phe Ile Pro Val Glu Ala Ile Arg Thr Val
          50               55               60

Ala Asn Val Ser Ile Xaa Asn Val Tyr Ile Lys Leu Ser Gly Lys Leu
          65               70               75               80

Arg Leu Ser Trp Ile Phe Gly Leu Pro Leu His Ile Ser Ser Asn Gly
          85               90               95

Asn Asp Gln Lys Cys Thr Gln Tyr Lys Pro Leu Phe Lys Thr Thr Pro
          100              105              110

Lys Thr Lys Gln Lys Trp Leu Arg Thr Thr Glu Arg Leu Leu Cys Val
          115              120              125

Pro Asp Val Lys Asp Gly Pro Arg Gly Tyr Leu His Gly Leu Asn Cys
          130              135              140

```


Glu Gly Lys Ile Lys Thr Ser Thr Ser Ile Ser Pro Glu Asp Leu Val
 145 150 155 160
 Cys Cys Glu Leu Ser Phe Val Glu Ser Asp Leu Val Ser Val Pro Leu
 165 170 175
 Cys Pro Ser Ile Gly Pro Leu Cys Ser Leu Leu Ala Phe Gly Leu Ser
 180 185 190
 Ser Gly Thr Ser Ala Phe Gly Leu Gly Leu Met Met Gly Leu Gln Lys
 195 200 205
 Leu Ser Ser Ser Phe Asp Phe Ala Thr Ile Ser Glu Thr Phe Thr Thr
 210 215 220
 Gly Ser Val Arg Leu Ser Leu Phe Cys Ala Phe Ile Leu Leu Phe Ser
 225 230 235 240
 Gln Leu Met Ala Ser Leu Ile His Phe Ser Thr Phe Ser Ile Ser Val
 245 250 255

Gly Ser

<210> 97
 <211> 478
 <212> DNA
 <213> Homo sapiens

<400> 97
 ggatccgggg tcgaagcagt tggattccat gatgggaagg ccattggcct ctcggtatatt 60
 cacaagcctc tcagcttcgc ggcgggacca ctctttcatc ctgtagtcag gcagataggc 120
 cacaaaagggtg ctgccaaagga ccaggatgat ggagacgcca aagaagaaga caagtcgcat 180
 gttccagacg tccaaaacgg ggtccttgtc ataaccatgg gagtctgggt tcttctcata 240
 caagttttcg tctcggggtt ctgggtcctc ttgccacggg gtggtcgggt ctggggggccg 300
 ctttcccgcc acagcggacg gggcgaccac agtcctggag aagctagatt cccagcggac 360
 gcgggcggcc gggagccctc gcgtcgccgc tgccgcaaaa agacggcgag cgctcaaacc 420
 aaacagccca gccgccatga cagatggtgc ttgcaggggt cgacgcggcc gcgaattc 478

<210> 98
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 98
 Asn Ser Arg Pro Arg Arg Pro Leu Gln Ala Pro Ser Val Met Ala Ala
 1 5 10 15

Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala Ala Ala Thr
 20 25 30

Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser Phe Ser Arg
 35 40 45

Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro Pro Glu Pro
50 55 60

Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu Asn Leu Tyr
65 70 75 80

Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro Val Leu Asp
85 90 95

Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser Ile Ile Leu
100 105 110

Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr Arg Met Lys
115 120 125

Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala
130 135 140

Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Gly Ser
145 150 155

<210> 99

<211> 258

<212> DNA

<213> Homo sapiens

<400> 99

ggatcctgag tagggcaata tctccaggca gaagtcccg aaatccaagc agcaggtgcc 60
aaggccagag cacgtcgggt ggcaggaaca tggcccgtcc agggcgccac agcgcatgga 120
gcagctctct tgggcatctg ctgtgggtcc ggggcccggt cggagggctg tcgccagcag 180
cagcagggcc cagggcagga gggctggctt catggtgcag cctgtgtctg cagccagcgt 240
cgacgcggcc gcaattc 258

<210> 100

<211> 86

<212> PRT

<213> Homo sapiens

<400> 100

Glu Phe Ala Ala Ala Ser Thr Leu Ala Ala Asp Thr Gly Cys Thr Met
1 5 10 15

Lys Pro Ala Leu Leu Pro Trp Ala Leu Leu Leu Ala Thr Ala Leu
20 25 30

Gly Pro Gly Pro Gly Pro Thr Ala Asp Ala Gln Glu Ser Cys Ser Met
35 40 45

Arg Cys Gly Ala Leu Asp Gly Pro Cys Ser Cys His Pro Thr Cys Ser
50 55 60

Gly Leu Gly Thr Cys Cys Leu Asp Phe Arg Asp Phe Cys Leu Glu Ile

65

70

75

80

Leu Pro Tyr Ser Gly Ser
85

<210> 101

<211> 664

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (524)..(662)

<223> N = A, C, G OR T/U

<400> 101

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ggatccctga aagtgaaca gaaagtacag catctgcacc aaattctcca agaacaccgt 60
taacacctcc gcctgcttct ggtgcttcca gtaccacaga tgtttgcagt gtatttgatt 120
ccgatcattc gagccctttt cactcaagca atgataccgt ctttatccaa gttactctgc 180
cccatggccc aagatctgct tctgtatcat ctataagttt aaccaaaaggc actgatgaag 240
tgctgtccc tctctctgtt cctccacgaa gacgaccaga atctgcccc gcagaatctt 300
caccatctaa gattatgtct aagcatttgg acagtcccc agccattcct cctaggcaac 360
ccacatcaaa agcctattca ccacgatatt caatatcaga ccggacctct atctcagacc 420
ctctgaaaag cctcccttta ttaccaccac gaaggaaaaa aaacctggag cactgtgttc 480
taactaccat cattccacct cccctttggg caaaaaggac atgnaatgct tnttccaaca 540
ggccttgccc ttacaccact ctctnaacac tttctacgac aagangattg catacacatg 600
ccagaagggn ctcttctgtg ggcgctgtct cngaaagatt taattctact ctcaaaactna 660
angg
664

```

<210> 102

<211> 207

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (1)..(43)

<223> XAA = ANYTHING

<400> 102

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Xaa Xaa Val Glu Asn Ile Phe Xaa Arg Gln Arg His Xaa Lys Xaa Pro
 1             5             10             15
Phe Trp His Val Tyr Ala Ile Xaa Leu Ser Lys Val Xaa Arg Glu Trp
      20             25             30
Cys Lys Gly Lys Ala Cys Trp Xaa Lys His Xaa Met Ser Phe Leu Pro
      35             40             45
Lys Gly Glu Val Glu Trp Leu Glu His Ser Ala Pro Gly Phe Phe Ser
      50             55             60
Phe Val Val Val Ile Arg Glu Gly Phe Gln Glu Gly Leu Arg Arg Ser

```

65

70

75

80

Gly Leu Ile Leu Asn Ile Val Val Asn Arg Leu Leu Met Trp Val Ala
 85 90 95

Glu Glu Trp Leu Gly Asp Cys Pro Asn Ala Thr Ser Met Val Lys Ile
 100 105 110

Leu Leu Gly Gln Ile Leu Val Val Phe Val Glu Glu Gln Glu Glu Gly
 115 120 125

Gln Ala Leu His Gln Cys Leu Trp Leu Asn Leu Met Ile Gln Lys Gln
 130 135 140

Ile Leu Gly His Gly Ala Glu Leu Gly Arg Arg Tyr His Cys Leu Ser
 145 150 155 160

Glu Lys Gly Ser Asn Asp Arg Asn Gln Ile His Cys Lys His Leu Trp
 165 170 175

Tyr Trp Lys His Gln Lys Gln Ala Glu Val Leu Thr Val Phe Leu Glu
 180 185 190

Asn Leu Val Gln Met Leu Tyr Phe Leu Phe His Phe Gln Gly Ser
 195 200 205

<210> 103

<211> 762

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> (464)..(746)

<223> N = A, C, G OR T.U

<400> 103

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ggatcccact gcaagcccca ccaggcggta ggggaagaag caggaggcca ggaaggcagc 60
ccagagcgcc acatacagct tctgtgtgat ctccggctgg acccacatga acaagttctt 120
gatcttctcc aggatgtcag ccatcttccc gaaaagggtt tgggctttct gggcgacgtc 180
cagcaccagc tggaacttct cagacacagt cagggtttcc tttggagggt ccacgggctc 240
agacacttcg ggcacgatgc tccactgtat ccgccacccc ctggcgatga ggtaattgag 300
ggataacctc agaattgcta gaaataagaa caatgggatg gcccagccat gccacacggc 360
attcatgtac acggtgaagg caatggcaga cgtgtagacg gagtaccagt cggataaggc 420
agagagggtt ttcacaaagt tagtgaccgg cttttggggg gggnacgct tgaccgctat 480
ttttagtaac ctgcggcgct caggggttcc tnttgtctcc acagtgtctc ctcggtgga 540
accgggaagt ccttccagct acttccccga accggttcgt aaaaccactt tttgcaggcc 600
ccgaggacag gcccttggtt tccggngct tntgntcca ttgntggcc tgggccctgc 660
cctttttggg ggcttggtt annccatctg ctntctcggg tntgggcctt nancacctt 720
ttggaccntt ttggttcaag ttncantcgg gccggttggc cg 762

```

<210> 104

<211> 253

<212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (6)..(99)
 <223> XAA = ANYTHING

<400> 104

Arg Pro Thr Gly Arg Xaa Xaa Thr Thr Lys Xaa Val Gln Glu Gly Xaa
 1 5 10 15

Xaa Gly Pro Xaa Pro Lys Xaa Gln Met Xaa Ser Thr Lys Pro Pro Lys
 20 25 30

Arg Ala Gly Pro Arg Pro Xaa Asn Gly Xaa Xaa Ser Xaa Arg Lys Pro
 35 40 45

Arg Ala Cys Pro Arg Gly Leu Gln Lys Val Val Leu Arg Thr Gly Ser
 50 55 60

Gly Lys Tyr Val Glu Gly Leu Pro Gly Ser Ser Arg Gly Asp Thr Val
 65 70 75 80

Glu Thr Xaa Gly Thr Pro Glu Arg Arg Arg Leu Leu Lys Ile Ala Val
 85 90 95

Lys Arg Xaa Pro Pro Gln Lys Pro Val Thr Asn Phe Val Lys Asn Leu
 100 105 110

Ser Ala Leu Ser Asp Trp Tyr Ser Val Tyr Thr Ser Ala Ile Ala Phe
 115 120 125

Thr Val Tyr Met Asn Ala Val Trp His Gly Trp Ala Ile Pro Leu Phe
 130 135 140

Leu Phe Leu Ala Ile Leu Arg Leu Ser Leu Asn Tyr Leu Ile Ala Arg
 145 150 155 160

Gly Trp Arg Ile Gln Trp Ser Ile Val Pro Glu Val Ser Glu Pro Val
 165 170 175

Glu Pro Pro Lys Glu Asp Leu Thr Val Ser Glu Lys Phe Gln Leu Val
 180 185 190

Leu Asp Val Ala Gln Lys Ala Gln Asn Leu Phe Gly Lys Met Ala Asp
 195 200 205

Ile Leu Glu Lys Ile Lys Asn Leu Phe Met Trp Val Gln Pro Glu Ile
 210 215 220

Thr Gln Lys Leu Tyr Val Ala Leu Trp Ala Ala Phe Leu Ala Ser Cys
 225 230 235 240

Phe Phe Pro Tyr Arg Leu Val Gly Leu Ala Val Gly Ser

<210> 105
 <211> 676
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> modified_base
 <222> (606)..(671)
 <223> N = A, C, G OR T/U

<400> 105
 ggatccaggc atgagttctg tcctttgaac tccatagtga ccccttttta ccttggtcca 60
 gatgaggaca ggtgtcggga ttccgatgac ctcacagctc aagtacacct gggcaccagt 120
 gacattccag atgtccttgg ggggcgtcac tatggaagga ccttgctcgc aggtgccctt 180
 gctgacctgg gtgatggcct tctccccgcg gctctcggcc ctctggctgg cggcgcgag 240
 ctggcagccg ctcggttagg tgggtgccgc gctgccgcac accgggtagc ggctccttga 300
 cagcacacag ccgcttacac cgggaccgcc ggctgctgcc ccggctttac ccttcgcgct 360
 cttgcggctc ttcacgcact ccattgcccg cgcgcagtag cccctgccgg cgccgccacc 420
 cccgcacggc tcgccctcgc cgcggggcgca catagggcag cagccgcacg cgtcgcggg 480
 ctgcgccagc aggcagccca gcggggggcag gggcgggcag gaggccggct cgcagggggc 540
 gcaggtgtcc gaagaggagg aagaggagag gggcaggagc aggagcagca gccagcgggc 600
 gccgangagc anggcgcgca acgacggccg cttcatggcg ggggtgcgggtg gcagcggtcn 660
 acnccggccgc naatta 676

<210> 106
 <211> 225
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (2)..(24)
 <223> XAA = ANYTHING

<400> 106
 Asn Xaa Arg Pro Xaa Xaa Pro Leu Pro Pro His Pro Ala Met Lys Arg
 1 5 10 15
 Pro Ser Leu Arg Ala Xaa Leu Xaa Gly Ala Ala Gly Leu Leu Leu
 20 25 30
 Leu Leu Pro Leu Ser Ser Ser Ser Ser Asp Thr Cys Gly Pro Cys
 35 40 45
 Glu Pro Ala Ser Cys Pro Pro Leu Pro Pro Leu Gly Cys Leu Leu Gly
 50 55 60
 Glu Thr Arg Asp Ala Cys Gly Cys Cys Pro Met Cys Ala Arg Gly Glu
 65 70 75 80
 Gly Glu Pro Cys Gly Gly Gly Gly Ala Gly Arg Gly Tyr Cys Ala Pro

85

90

95

Gly Met Glu Cys Val Lys Ser Arg Lys Arg Arg Lys Gly Lys Ala Gly
 100 105 110

Ala Ala Ala Gly Gly Pro Gly Val Ser Gly Val Cys Val Cys Lys Ser
 115 120 125

Arg Tyr Pro Val Cys Gly Ser Asp Gly Thr Thr Tyr Pro Ser Gly Cys
 130 135 140

Gln Leu Arg Ala Ala Ser Gln Arg Ala Glu Ser Arg Gly Glu Lys Ala
 145 150 155 160

Ile Thr Gln Val Ser Lys Gly Thr Cys Glu Gln Gly Pro Ser Ile Val
 165 170 175

Thr Pro Pro Lys Asp Ile Trp Asn Val Thr Gly Ala Gln Val Tyr Leu
 180 185 190

Ser Cys Glu Val Ile Gly Ile Pro Thr Pro Val Leu Ile Trp Asn Lys
 195 200 205

Val Lys Arg Gly His Tyr Gly Val Gln Arg Thr Glu Leu Met Pro Gly
 210 215 220

Ser
 225

<210> 107

<211> 267

<212> DNA

<213> Homo sapiens

<400> 107

ggatcctgta gccgtgatgg tggctcgagg agcaatccag tgcacagtaa aagagttggc 60
 agtaatatca gaaaagtcaa tgccagttgg ggaatcaaga cctgttttct gtcttcctct 120
 aagaggtgtg ctctcatggt gtctctagac actggagaca ctcaactacat attctgtacc 180
 aggcaggaga tttgttaaga ccaactgcatt gtctgaagga gaaattgaca actctgcaac 240
 atcttccgtc gacgcggccg cgaattc 267

<210> 108

<211> 89

<212> PRT

<213> Homo sapiens

<400> 108

Glu Phe Ala Ala Ala Ser Thr Glu Asp Val Ala Glu Leu Ser Ile Ser
 1 5 10 15

Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu Pro Gly Thr Glu
 20 25 30

Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln His Glu Ser Thr Pro
35 40 45

Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp Ser Pro Thr Gly Ile Asp
50 55 60

Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr Val His Trp Ile Ala Pro
65 70 75 80

Arg Ala Thr Ile Thr Ala Thr Gly Ser
85

<210> 109
<211> 911
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (659)..(911)
<223> N = A, C, G OR T/U

<400> 109
ggatccgccca gtgaggttgc gccagtaggc aggggaagtcc tgggaactgga aggtgtagac 60
ggcgatgagg accagcatgg tgtaggccac cacgagccac cagaaggcct tgagcagctt 120
ccgccacagg ctgtagtaga cctggaagag ggtgaggcag agcaggaaga ggaacatgta 180
gacaatcttg tagaccacga ggcggccggc gaagctgacc acgatgaaca tgccagcaca 240
cacatagatc cagtacttgg cgtacacgcc cttcaccagc tcccccaggc tctgcaacag 300
cgtctgcgtc cgcgtgggct ctgtgtctgc cacggtgacc tccgtcagcg cagctggaga 360
ctctgcccac ttcagcagct tctctttcac aaactggcgc agcaggagcc agaaggtcag 420
ggtgtagagc aacatggcac caaggtccag acaggggtag cgggtgtgct ccagccccag 480
ctggcgcagg ctgacggggc ccagggtggt gggcagctca gggcgcaggc ccatggccca 540
cacgtagcgt aggcagcaca gcgtcatccc atacagcagg atgcagggcg agcacagcat 600
ggccagtttg tggcggctgc gcaccgtcca gatgaggcag gccagagcag cagtacgaan 660
gtcagccagc tgtggttaggt gatgctncat accatcatgg caatgagcgc gcacacatag 720
ctttgggtcc atgatgangg gggcccaggc tggggaacgg aaacncctnc ctgggctanc 780
ccncttgggc ccacagggcn ccccaggagg gaactttgnc cgtcaattct gcncaaagca 840
tttnacatt cggggtcggg ngctggggna ccactgntgt aaantccctt tctggggccc 900
tgtncacntt n 911

<210> 110
<211> 302
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (1)..(83)
<223> XAA = ANYTHING

<400> 110
Xaa Xaa Thr Gly Pro Gln Lys Gly Xaa Leu Xaa Gln Trp Xaa Pro Ser
1 5 10 15

Xaa Arg Pro Arg Arg Xaa Xaa Cys Phe Xaa Gln Asn Arg Xaa Lys Phe
20 25 30
Pro Pro Gly Xaa Ala Cys Gly Pro Lys Xaa Xaa Ser Pro Gly Arg Xaa
35 40 45
Phe Arg Ser Pro Ala Trp Ala Pro Xaa Ile Met Asp Pro Lys Leu Cys
50 55 60
Val Arg Ala His Cys His Asp Gly Met Xaa His His Leu Pro Gln Leu
65 70 75 80
Ala Asp Xaa Arg Thr Ala Ala Leu Ala Cys Leu Ile Trp Thr Val Arg
85 90 95
Ser Arg His Gln Leu Ala Met Leu Cys Ser Pro Cys Ile Leu Leu Tyr
100 105 110
Gly Met Thr Leu Cys Cys Leu Arg Tyr Val Trp Ala Met Asp Leu Arg
115 120 125
Pro Glu Leu Pro Thr Thr Leu Gly Pro Val Ser Leu Arg Gln Leu Gly
130 135 140
Leu Glu His Thr Arg Tyr Pro Cys Leu Asp Leu Gly Ala Met Leu Leu
145 150 155 160
Tyr Thr Leu Thr Phe Trp Leu Leu Leu Arg Gln Phe Val Lys Glu Lys
165 170 175
Leu Leu Lys Trp Ala Glu Ser Pro Ala Ala Leu Thr Glu Val Thr Val
180 185 190
Ala Asp Thr Glu Pro Thr Arg Thr Gln Thr Leu Leu Gln Ser Leu Gly
195 200 205
Glu Leu Val Lys Gly Val Tyr Ala Lys Tyr Trp Ile Tyr Val Cys Ala
210 215 220
Gly Met Phe Ile Val Val Ser Phe Ala Gly Arg Leu Val Val Tyr Lys
225 230 235 240
Ile Val Tyr Met Phe Leu Phe Leu Leu Cys Leu Thr Leu Phe Gln Val
245 250 255
Tyr Tyr Ser Leu Trp Arg Lys Leu Leu Lys Ala Phe Trp Trp Leu Val
260 265 270
Val Ala Tyr Thr Met Leu Val Leu Ile Ala Val Tyr Thr Phe Gln Phe
275 280 285
Gln Asp Phe Pro Ala Tyr Trp Arg Asn Leu Thr Gly Gly Ser
290 295 300

<210> 111
 <211> 818
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (701)..(817)
 <223> N = A, C, G OR T/U

<400> 111
 ggatccaggg acaatgttgt cacaatagca aaaagcaaata ttaggataa tacaatatag 60
 aaatttccca gccaatataa ccttccaaag tcgccaagta gatcaaatac agtgattccc 120
 agtgttctcg acatcacagg cagagcagag ctcaaaacca agatggacac acaatttcca 180
 atgatctttg tcatagtgtg gtcattcttc ttgggagtaa agtttccaaa aaatcgaagg 240
 ctatagaagc cgacaacaga ggacaccata agatagaaaa tcaaaatgat ttcaagcgca 300
 gctcccacaa aaccaaactg agaaagagag gcatttccta ttccaggccc ccttggtcct 360
 tttggcattg ctgtttcatc aaccaatagg caaagaatat tacaagccac caagaggacc 420
 gagatggatg tctcaataag aaggagaacc ataacagcgg gatacaccaa atttctttcc 480
 catgctgaag ccttttttgc cctctctaata tttgtcttaa gagtctttac attttcaagt 540
 tcttggtcca actccattat gttgtattcc accgatgaag acagcccatt tagtcgtctc 600
 tggagtgtt cttcctctaa ggtaatgata taaatttggt catccagggtc ttcagaattg 660
 ttggcttcac tagcaactga cccatcactg tgaactacga naaanggcaa ctggtgtacn 720
 caaganaagt aacaacntcc atcatgattt caggatntaa tagggagatg nactnccana 780
 atcatttaag atnctgcttg cggatcgttg gcatgang 818

<210> 112
 <211> 254
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (8)..(38)
 <223> XAA = ANYTHING

<400> 112
 Ser Cys Gln Arg Ser Ala Ser Xaa Ile Leu Asn Asp Xaa Gly Ser Xaa
 1 5 10 15
 Ser Pro Tyr Xaa Ile Leu Lys Ser Trp Xaa Leu Leu Leu Xaa Leu Xaa
 20 25 30
 Thr Pro Val Ala Xaa Xaa Arg Ser Ser Gln Trp Val Ser Cys Ser Gln
 35 40 45
 Gln Phe Arg Pro Gly Thr Asn Leu Tyr His Tyr Leu Arg Gly Arg Ser
 50 55 60
 Thr Pro Glu Thr Thr Lys Trp Ala Val Phe Ile Gly Gly Ile Gln His
 65 70 75 80
 Asn Gly Val Gly Thr Arg Thr Lys Cys Lys Asp Ser Asp Lys Ile Arg

85

90

95

Glu Ala Lys Lys Gly Phe Ser Met Gly Lys Lys Phe Gly Val Ser Arg
 100 105 110

Cys Tyr Gly Ser Pro Ser Tyr Asp Ile His Leu Gly Pro Leu Gly Gly
 115 120 125

Leu Tyr Ser Leu Pro Ile Gly Asn Ser Asn Ala Lys Arg Asn Lys Gly
 130 135 140

Ala Trp Asn Arg Lys Cys Leu Ser Phe Tyr Val Trp Phe Cys Gly Ser
 145 150 155 160

Cys Ala Asn His Phe Asp Phe Leu Ser Tyr Gly Val Leu Cys Cys Arg
 165 170 175

Leu Leu Pro Ser Ile Phe Trp Lys Leu Tyr Ser Gln Glu Arg His Asn
 180 185 190

Tyr Asp Lys Asp His Trp Lys Leu Cys Val His Leu Gly Phe Glu Leu
 195 200 205

Cys Ser Ala Cys Asp Val Glu Asn Thr Gly Asn His Ile Ser Thr Trp
 210 215 220

Arg Leu Trp Lys Val Leu Ala Gly Lys Phe Leu Tyr Cys Ile Ile Leu
 225 230 235 240

Gln Phe Ala Phe Cys Tyr Cys Asp Asn Ile Val Pro Gly Ser
 245 250

<210> 113

<211> 905

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (708)..(900)

<223> N = A, C, G OR T/U

<400> 113

ggatccattg gggttttgggg ggaagaggaa gactgacggt cccccagga gttcaggtgc 60
 tgggcacggt gggcatgtgt gagttttgtc acaagatttg ggctcaactc tcttgtccac 120
 cttggtgttg ctgggcttgt gattcacgtt gcagatgtag gtctgggtgc ccaagctgct 180
 ggagggcacg gtcaccacgc tgctgagggg gtagagtcc gaggactgta ggacagccgg 240
 gaaggtgtgc acgccgtgg tcagggcgcc tgagttccac gacaccgtca ccggttcggg 300
 gaagtagtcc ttgaccaggc agcccagggc cgtgtgtgcc ccagaggtgc tcttggagga 360
 ggggtgccagg gggaagaccg atggggccctt ggtggaggct gaggagacgg tgaccagggt 420
 accctggccc cactggtaac ttgtagccat ctccgcaagt ctcgcacagt aatacatggc 480
 ggtgtccgag gccttcaggc tgctccactg caggtaggag gtactgatgg acttgtcgac 540
 tgacatggtg acctggcctt ggaaggacgg gctgtatgtg gcatcagagt caccaggata 600
 gatgatcccc atccactcca gacccttccc gggcatctgg cgcaccagg cgatccagta 660

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actggagaag tagtatccag agcccttaca ggagatcttc agagactncc cgggcttttt 720
cacctntggt ccagactgca cagctgcacc tcggacanac tccttggana acaaccagaa 780
ganggccagg atggcngctg acccctgatg ggganggaan aaatgaaccc tgggtcaancg 840
gcngnaattn ancttactnt tcttttnatt aaaaaactct tnaaaagcna tnaaagcatn 900
ccttc
905

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<210> 114
<211> 301
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (2)..(66)
<223> XAA = ANYTHING

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```

<400> 114
Arg Xaa Ala Xaa Xaa Ala Phe Xaa Glu Phe Phe Asn Xaa Lys Xaa Ser
 1              5              10              15

Lys Xaa Asn Xaa Xaa Arg Leu Thr Arg Val His Xaa Phe Xaa Pro His
          20              25              30

Gln Gly Ser Ala Ala Ile Leu Ala Xaa Phe Trp Leu Xaa Ser Lys Glu
 35              40              45

Xaa Val Arg Gly Ala Ala Val Gln Ser Gly Pro Xaa Val Lys Lys Pro
 50              55              60

Gly Xaa Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Tyr Phe Ser
 65              70              75              80

Ser Tyr Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
          85              90              95

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ala Thr Tyr Ser Pro
 100              105              110

Ser Phe Gln Gly Gln Val Thr Met Ser Val Asp Lys Ser Ile Ser Thr
 115              120              125

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 130              135              140

Tyr Cys Ala Arg Leu Ala Glu Met Ala Thr Ser Tyr Gln Trp Gly Gln
 145              150              155              160

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
          165              170              175

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 180              185              190

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser

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195	200	205
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val		
210	215	220
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro		
225	230	235 240
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys		
	245	250 255
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp		
	260	265 270
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly		
	275	280 285
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Asn Gly Ser		
	290	295 300

<210> 115
 <211> 458
 <212> DNA
 <213> Homo sapiens

<400> 115
 ggatccggct ctgaccttct ccacgtcggc ccgggccgctc tggtaattgt ccacgctgcc 60
 tgggatgtag gagcactgct ggttctggtc ccgagtgtcc tccgtgtggt acagcacagc 120
 ccacctgccg gcagctgaca cgttgacca caggcatggg tactggggca ctttcttgcc 180
 cttcagctcc tcttggtccc tgatgttggt ctcaatcagg tggcacttgg attcctgggt 240
 ccacacgctt ttctggtaga ggggcagcac agtcgtgacc aggatgtagt aggtgatgac 300
 ggcacacacc accatggta caccaggca aagggtcgt gtctctcccc gcttctgggc 360
 catcaccagc ttcttcacca tattcactgg gggcagtgat catttagtct tcccggcgctc 420
 ctgtgggtct tgagcagcgt cgacgcggcc gcgaattc 458

<210> 116
 <211> 151
 <212> PRT
 <213> Homo sapiens

<400> 116
 Ile Arg Gly Arg Val Asp Ala Ala Gln Asp Pro Gln Asp Ala Gly Lys
 1 5 10 15
 Thr Lys Ser Leu Pro Pro Val Asn Met Val Lys Lys Leu Val Met Ala
 20 25 30
 Gln Lys Arg Gly Glu Thr Arg Ala Leu Cys Leu Gly Val Thr Met Val
 35 40 45
 Val Cys Ala Val Ile Thr Tyr Tyr Ile Leu Val Thr Thr Val Leu Pro
 50 55 60

Leu Tyr Gln Lys Ser Val Trp Thr Gln Glu Ser Lys Cys His Leu Ile
 65 70 75 80
 Glu Thr Asn Ile Arg Asp Gln Glu Glu Leu Lys Gly Lys Lys Val Pro
 85 90 95
 Gln Tyr Pro Cys Leu Trp Val Asn Val Ser Ala Ala Gly Arg Trp Ala
 100 105 110
 Val Leu Tyr His Thr Glu Asp Thr Arg Asp Gln Asn Gln Gln Cys Ser
 115 120 125
 Tyr Ile Pro Gly Ser Val Asp Asn Tyr Gln Thr Ala Arg Ala Asp Val
 130 135 140
 Glu Lys Val Arg Ala Gly Ser
 145 150

<210> 117
 <211> 715
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (669)..(710)
 <223> N = A, C, G OR T/U

<400> 117
 ggatcctgct tccaggcgct tctcattctc atggatcttc ttcacccgca gcttctgctt 60
 ctcagtcaga aggttggtgt cctcatccct ctcatacagg gtgaccagga cgttcttgag 120
 ccagtccgcg atgcgcaggg ggaattcggc cagctcagag tccaggcaag gggggatgta 180
 tttgcaaggc ccgatgtagt ccaggtggag cttgtggccc ttcttggtgc cctccagggt 240
 gcactttgtg gcaaagaagt ggcaggaaga gtcgaaggtc ttgttgatcat tgctgcacac 300
 cttctcaaac tcgccaatgg gggctgggca gctgggtggg tcttggcaca cgcacatggg 360
 ggtgttggtc tcatccagct cgcacacctt gccgtgtttg cagtgggtgg tctggcaggg 420
 attttccgcc accacctcct cttcgggttt ctctgcacca tcatcaaatt ctcctacttc 480
 cacctggaca ggattagctc ccacagatac ctcagtcacc tctgccacag tttcttccac 540
 cacctctgtc tcatcaggca gggcttcttg ctgagggggt gccaaaggccc tcccggccag 600
 gcaaaggaga aagaagatcc aggcctcat ggtgctggga accctcagtg gcaggcaggc 660
 aggcggcgang canancgcgc tctccgggca gtctggtcga cncggccgcn aattc 715

<210> 118
 <211> 238
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (2)..(16)
 <223> XAA = ANYTHING

<400> 118

Asn Xaa Arg Pro Xaa Arg Pro Asp Cys Pro Glu Ser Ala Xaa Cys Xaa
 1 5 10 15
 Pro Pro Ala Cys Leu Pro Leu Arg Val Pro Ser Thr Met Arg Ala Trp
 20 25 30
 Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala Pro Gln
 35 40 45
 Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr Val Ala
 50 55 60
 Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val Glu Val
 65 70 75 80
 Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val Val Ala
 85 90 95
 Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val Cys Glu
 100 105 110
 Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro Thr Ser
 115 120 125
 Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn Asp Asn
 130 135 140
 Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys Thr Leu
 145 150 155 160
 Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile Gly Pro
 165 170 175
 Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu Phe Pro
 180 185 190
 Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu Tyr Glu
 195 200 205
 Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu Arg Val
 210 215 220
 Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Ser
 225 230 235

<210> 119

<211> 467

<212> DNA

<213> Homo sapiens

<400> 119

ggatcccttg tgggtccgccca ctccgaggtta tccgtccagt ggccgcgggtc ccgcggggac 60
 cccggggcgc tgcctgggtgc tgccttccgc cgcgggctgc gagctgccgg tggccgacgc 120
 ctgctgctgc tgttgctgct gctgctgctg ctgctgcggg ggccgctcct tctggccgcc 180

```

gaggctgctg tacactagca acaagctggt gcacatggtg gtgagcgcta aacacactgc 240
cagaccatgg cgcacaggg tcttcatttt gggcacctct tttgtgcaga atcctcaggc 300
tcgcgcgtcc ggggccactt tttcctggag ggtttccatg atgggtaatg gggcggaggc 360
ggctctgatt tttgccagc agccggccgc ggcagatcgc gcgcgggagc cgcgggaccc 420
gggaagcgcg gctgttgcag agattaggtc gacgcggccg cgaattc 467

```

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<210> 120
<211> 154
<212> PRT
<213> Homo sapiens

```

```

<400> 120
Ile Arg Gly Arg Val Asp Leu Ile Ser Ala Thr Ala Ala Leu Pro Gly
 1             5             10             15
Ser Arg Gly Ser Arg Ala Arg Ser Ala Ala Ala Gly Cys Trp Ala Lys
      20             25             30
Ile Arg Ala Ala Ser Ala Pro Leu Pro Ile Met Glu Thr Leu Gln Glu
      35             40             45
Lys Val Ala Pro Asp Ala Arg Ala Gly Phe Cys Thr Lys Glu Val Pro
      50             55             60
Lys Met Lys Thr Leu Met Arg His Gly Leu Ala Val Cys Leu Ala Leu
      65             70             75             80
Thr Thr Met Cys Thr Ser Leu Leu Leu Val Tyr Ser Ser Leu Gly Gly
      85             90             95
Gln Lys Glu Arg Pro Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln
      100             105             110
Gln Gln Ala Ser Ala Thr Gly Ser Ser Gln Pro Ala Ala Glu Ser Ser
      115             120             125
Thr Gln Gln Arg Pro Gly Val Pro Ala Gly Pro Arg Pro Leu Asp Gly
      130             135             140
Tyr Leu Gly Val Ala Asp His Lys Gly Ser
145             150

```

```

<210> 121
<211> 859
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> modified_base
<222> (677)..(857)
<223> N = A, C, G, OR T/U

```

```

<400> 121

```



```

ggatccacac acatcctcac cccacagnaa actgctggac aactgaaga aactgaataa 60
aacagatgaa gaaataagca gttaaaaaaa taagtcgccc ctccaaaaca cgcccccatc 120
ccacagcgct ccgcagcttc ccaccaccgc ccgcctcagt tcctttgcgt ctggtgcctc 180
cccagccctg cagccctggg ctggcactgt tgccgctgca ttctcgtgtt cagtgatgcc 240
ctcttcttgt ttgaaacaaa agaaaataat gcatttgtgt ttttaaaaag agtatcttat 300
acatgtatcc taaaaagaga agctcatgtg caattggtgc acagcaggag aaatttctgg 360
actgttagga tgaatggacg ccttctcccc gttatttaag atttgtgacc ttgtacataa 420
ccctgggtga cgtgcacatt gcttgggtat ggaacggtag aaatttgggt gtttttaaaa 480
ccttgtttgg ggttgttcct gtccttgttg agaatacatag agatgtctgt gttcttggag 540
tatttcacac tgaggactaa tctgctatct tcattccagt ccctaccctt cagtgcctgc 600
tctcatccaa ataacctggg aggtgacaat caggatatct caggagggtc aaggtggaac 660
agacctcttt gccttttcca gcgtctcata ccccggtag tgcantgtg ggtggaggct 720
ggggtgtctg caccaantca gggcagcgtc ctnttccna gcctgtactg gcccttccc 780
ancctgggtc cccagggctg ggatccccag ggantncttc cntttaanna aagggccctg 840
acngggaaaa acaactncc                                     859

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<210> 122
<211> 278
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> MOD_RES
<222> (1)..(61)
<223> XAA = ANYTHING

```

```

<400> 122
Xaa Val Val Phe Pro Xaa Gln Gly Pro Xaa Xaa Lys Xaa Lys Xaa Ser
 1             5             10             15
Leu Gly Ile Pro Ala Leu Gly Thr Gln Xaa Gly Lys Gly Pro Val Gln
          20             25             30
Ala Xaa Lys Xaa Asp Ala Ala Leu Xaa Trp Cys Arg His Pro Ser Leu
          35             40             45
His Pro Gln Xaa His Tyr Arg Gly Tyr Glu Thr Leu Xaa Lys Ala Lys
          50             55             60
Arg Ser Val Pro Pro Trp Thr Ser Asp Ile Leu Ile Val Thr Ser Gln
          65             70             75             80
Val Ile Trp Met Arg Ala Gly Thr Glu Gly Gly Leu Glu Arg Gln Ile
          85             90             95
Ser Pro Gln Cys Glu Ile Leu Gln Glu His Arg His Leu Tyr Asp Ser
          100            105            110
Gln Gln Gly Gln Glu Gln Pro Gln Thr Arg Phe Lys His Pro Asn Phe
          115            120            125
Tyr Arg Ser Ile Pro Lys Gln Cys Ala Arg His Pro Gly Leu Cys Thr
          130            135            140

```

Arg Ser Gln Ile Leu Asn Asn Gly Glu Lys Ala Ser Ile His Pro Asn
145 150 155 160

Ser Pro Glu Ile Ser Pro Ala Val His Gln Leu His Met Ser Phe Ser
165 170 175

Phe Asp Thr Cys Ile Arg Tyr Ser Phe Lys Thr Gln Cys Ile Ile Phe
180 185 190

Phe Cys Phe Lys Gln Glu Glu Gly Ile Thr Glu His Glu Asn Ala Ala
195 200 205

Ala Thr Val Pro Ala Arg Ala Cys Arg Ala Gly Glu Ala Thr Asp Ala
210 215 220

Lys Glu Leu Arg Arg Ala Val Val Gly Ser Cys Gly Ala Leu Trp Asp
225 230 235 240

Gly Gly Val Phe Trp Arg Gly Asp Leu Phe Phe Leu Leu Ile Ser Ser
245 250 255

Ser Val Leu Phe Ser Phe Phe Ser Val Ser Ser Ser Xaa Leu Trp Gly
260 265 270

Glu Asp Val Cys Gly Ser
275

<210> 123
<211> 478
<212> DNA
<213> Homo sapiens

<400> 123
ggatccatca tatgtgtcta ctgtggggac aactggagtg aaaacttcgg ttgctggcag 60
gtccgtggga aaatcagtga ccagttcatc agattcatca gaatgggtgag actcatcaga 120
ctggtgagaa tcatcagtgt catctacatc atcagagtcg tttgagtcaa tggagtcctg 180
gctgtccaca tggatcatcat catcttcatc atccatatca tccatgtggg catggctttc 240
gttggaactta cttggaaggg tctgtggggc taggagattc tgcttctgag atgggtcagg 300
gtttagccat gtggccacag catctgggta tttgttgtaa agctgctttt cctcagaact 360
tccagaatca gcctgtttaa ctggtatggc acaggtgatg cctaggaggc aaaagcaaact 420
cactggtcga cgcggccgcg aattcgcggc cgcgtcgacg tcgacgcgc gcgaattc 478

<210> 124
<211> 159
<212> PRT
<213> Homo sapiens

<400> 124
Asn Ser Arg Arg Val Asp Val Asp Ala Ala Ala Asn Ser Arg Pro Arg
1 5 10 15

Arg Pro Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala Ile Pro
20 25 30

Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu Tyr Asn
35 40 45

Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro Ser Gln
50 55 60

Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser Asn Glu
65 70 75 80

Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His
85 90 95

Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp
100 105 110

Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu
115 120 125

Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu
130 135 140

Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Ser
145 150 155

<210> 125
<211> 889
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (743)..(888)
<223> N = A, C, G OR T/U

<400> 125
ggatccgctt ttgtgtgcaa acaatggcaa acaatggcag caaaccacag cccagctgac 60
agccattaag atggagtatt catttgtcat ggtgggtaaa ggctcttcaa tagctgctaa 120
tcaaaataga gaaaaatgaa tgtatggcac gatgcaactc taataagact ggggtgtccaa 180
atgagtgact ccacataggt atgcgtaagg cgtacatgga atgaccttct ctttgaactt 240
gctgccaccg tggagcagca tatctccctt gagaacttcc tcccttgact tccgaggaga 300
tcttactctc tcatttctga ccgaccttcc ttacacctgt tcttcccacc cattccctca 360
atgagacagt cccccagcca ctgctctctg ttcaaattcc ctgctgact gatgccctgg 420
ggaagatccc ttctcctaaa tcttatgggg atttaagaat attactgtc cagctgcagc 480
caaagtggac atggcattgg gacgcagatg tgcttgctgt tacctaaata ctattctaa 540
agatggcaaa gactgggact ttcattgtatt catttccgac actctcattc ccagatactg 600
agctagaagc tggatgagca gatacaagac tgggtgttccc aaggaactta aaaaaccatc 660
ctccctgtca ctgtagtggc tgccatgggt tgactatacc aagtactctg ctaactgctt 720
tacttatgca atcccaccta atnctcacag caaccagtg aggnnggctac taggataatt 780
ccttttccct ttcttttttt tttttttttg anacggattt nctnttggtg cccagctgga 840
ggcaangggc gaactcgggt actgaaaccc ctntctctngg gtnancnt 889

<210> 126

<211> 285
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(47)
 <223> XAA = ANYTHING

<400> 126

Xaa	Xaa	Thr	Xaa	Glu	Xaa	Gly	Phe	Gln	Pro	Ser	Ser	Pro	Xaa	Ala	Ser	1	5	10	15
Ser	Trp	Ala	Thr	Xaa	Xaa	Asn	Pro	Xaa	Gln	Lys	Lys	Lys	Lys	Arg	Lys	20	25	30	
Arg	Lys	Arg	Asn	Tyr	Pro	Ser	Ser	Xaa	Leu	Thr	Gly	Leu	Leu	Xaa	Leu	35	40	45	
Gly	Gly	Ile	Ala	Val	Lys	Gln	Leu	Ala	Glu	Tyr	Leu	Val	Ser	Thr	His	50	55	60	
Gly	Ser	His	Tyr	Ser	Asp	Arg	Glu	Asp	Gly	Phe	Leu	Ser	Ser	Leu	Gly	65	70	75	80
Thr	Pro	Val	Leu	Tyr	Leu	His	His	Gln	Leu	Leu	Ala	Gln	Tyr	Leu	Gly	85	90	95	
Met	Arg	Val	Ser	Glu	Met	Asn	Thr	Lys	Ser	Gln	Ser	Leu	Pro	Ser	Leu	100	105	110	
Glu	Val	Phe	Arg	Ala	Gln	Ala	His	Leu	Arg	Pro	Asn	Ala	Met	Ser	Thr	115	120	125	
Leu	Ala	Ala	Ala	Gly	Gln	Val	Ile	Phe	Leu	Asn	Pro	His	Lys	Ile	Glu	130	135	140	
Lys	Gly	Ser	Ser	Pro	Gly	His	Gln	Ser	Arg	Arg	Glu	Phe	Glu	Gln	Arg	145	150	155	160
Ala	Val	Ala	Gly	Gly	Leu	Ser	His	Gly	Asn	Gly	Trp	Glu	Glu	Gln	Gly	165	170	175	
Lys	Glu	Arg	Ser	Val	Arg	Asn	Glu	Arg	Val	Arg	Ser	Pro	Arg	Lys	Ser	180	185	190	
Arg	Glu	Glu	Val	Leu	Lys	Gly	Asp	Met	Leu	Leu	His	Gly	Gly	Ser	Lys	195	200	205	
Phe	Lys	Glu	Lys	Val	Ile	Pro	Cys	Thr	Pro	Tyr	Ala	Tyr	Leu	Cys	Gly	210	215	220	
Val	Thr	His	Leu	Asp	Thr	Gln	Ser	Tyr	Ser	Cys	Ile	Val	Pro	Tyr	Ile	225	230	235	240

His Phe Ser Leu Phe Leu Ala Ala Ile Glu Glu Pro Leu Pro Thr Met
 245 250 255

Thr Asn Glu Tyr Ser Ile Leu Met Ala Val Ser Trp Ala Val Val Cys
 260 265 270

Cys His Cys Leu Pro Leu Phe Ala His Lys Ser Gly Ser
 275 280 285

<210> 127
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 127
 ggatccctca acgccggtgg tttcttggtc ggtgggtgac tctgagccgt cggggcagac 60
 gggacagcac tcgccctcgg ggacttcggc gccggggcag ttcttggtct cgtcacagat 120
 cactcatcgc cacaacacct tgccgttgtc gcagacgcag atccggcagg gctcgggttt 180
 ccacacgtct cggtcattgt acctgaggcc gttctgtacg caggtgattg gtgggatgtc 240
 ttctgtttgg cctcgcactt ggccctcttc ttggccgtgc gtcaggaggg cgggtggccgc 300
 taagaggagc aggagccgga gtcgacgcgg ccgcgaatt 339

<210> 128
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 128
 Asn Ser Arg Pro Arg Arg Leu Arg Leu Leu Leu Leu Leu Ala Ala Thr
 1 5 10 15
 Ala Leu Leu Thr His Gly Gln Glu Glu Gly Gln Val Glu Gly Gln Asp
 20 25 30
 Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn Gly Leu Arg Tyr His
 35 40 45
 Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg Ile Cys Val Cys Asp
 50 55 60
 Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys Asp Glu Thr Lys Asn
 65 70 75 80
 Cys Pro Gly Ala Glu Val Pro Glu Gly Glu Cys Cys Pro Val Cys Pro
 85 90 95
 Asp Gly Ser Glu Ser Pro Thr Asp Gln Glu Thr Thr Gly Val Glu Gly
 100 105 110
 Ser

<210> 129
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 129
 ggatccatag caggggggctg ggcgctggtt gggcccaaag agatgcaagt cgccgtattc 60
 ccatagaaac agctgagtca tcagggctcc gaagcccaca accgccagaa tgaggaccag 120
 caggaccag cgggctttct tttccgcagc cttccacgcc tcaatctcat tcatgggcag 180
 ctcatggcg ggctcctctg caggcacctt cagtccttg tacatcagtt taggcttcat 240
 cttccctcaa ggctggggga tacgcagagc ccaggtgaga aggtgggtgt gtcaggggtct 300
 ccaaaccctg aggggcctcg gcctcgctct caggcgtctg ctgctacctc cgctgggccc 360
 cagcttctgt ctggacaggc tgaacgaggg tgggaggagg gggcggggcc tgtgggagct 420
 ccgcccactg cagcggggag tctgcgcagt gcgtgcccga gtccgggctc accgcagcga 480
 gaagcggggc tcggctcccc agacacggtc gtcacaggtc gacgcggccg cgaattc 537

<210> 130
 <211> 176
 <212> PRT
 <213> Homo sapiens

<400> 130
 Glu Phe Ala Ala Ala Ser Thr Trp Ser Asp Arg Val Trp Gly Ala Glu
 1 5 10 15
 Pro Arg Phe Ser Leu Arg Ala Arg Thr Gly Ala Arg Thr Ala Gln Thr
 20 25 30
 Pro Arg Cys Ser Gly Arg Ser Ser His Arg Pro Arg Pro Leu Leu Pro
 35 40 45
 Pro Ser Phe Ser Leu Ser Arg Gln Lys Leu Gly Pro Ser Gly Gly Ser
 50 55 60
 Ser Arg Arg Leu Arg Ala Arg Pro Arg Pro Leu Arg Val Trp Arg Pro
 65 70 75 80
 His Thr His Leu Leu Thr Trp Ala Leu Arg Ile Pro Gln Pro Gly Lys
 85 90 95
 Met Lys Pro Lys Leu Met Tyr Gln Glu Leu Lys Val Pro Ala Glu Glu
 100 105 110
 Pro Ala Asn Glu Leu Pro Met Asn Glu Ile Glu Ala Trp Lys Ala Ala
 115 120 125
 Glu Lys Lys Ala Arg Trp Val Leu Leu Val Leu Ile Leu Ala Val Val
 130 135 140
 Gly Phe Gly Ala Leu Met Thr Gln Leu Phe Leu Trp Glu Tyr Gly Asp
 145 150 155 160
 Leu His Leu Phe Gly Pro Asn Gln Arg Pro Ala Pro Cys Tyr Gly Ser
 165 170 175

<210> 131
 <211> 392
 <212> DNA
 <213> Mus musculus
 <220>
 <221> modified_base
 <222> (9)..(354)
 <223> N = A, C G OR T/U

<400> 131
 gaattcggnc agtggcccgnc aggaatncgg ncccggggga acctttcctg agattctgcc 60
 ccaggatgcc aactttgant nggatgaana ctacaacttg tnccttctc atctgcactc 120
 ccctgctcca gctgatggtc ccagtgaata ctgatgagac catagagatt atcgtggaga 180
 ataagggtcaa ggaacttctt gccaatccag ctaactatcc ctccactgta acgaanactc 240
 tctcttgac tagtgtaag actatgaaca gatgggcctc ctgccctgct gggatgactg 300
 ctactgggtg tgcttggtgc tttgcctgtg gatcttgga gatccagagt gganatactt 360
 gcaactgcct gtgcttactc ctgactggat cc 392

<210> 132
 <211> 130
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (3)..(118)
 <223> XAA = ANYTHING

<400> 132
 Ile Arg Xaa Val Ala Arg Arg Asn Xaa Xaa Pro Gly Glu Pro Phe Leu
 1 5 10 15
 Arg Phe Cys Pro Arg Met Pro Thr Leu Xaa Xaa Met Xaa Thr Thr Thr
 20 25 30
 Cys Xaa Leu Leu Ile Cys Ile Ser Leu Leu Gln Leu Met Val Pro Val
 35 40 45
 Asn Thr Asp Glu Thr Ile Glu Ile Ile Val Glu Asn Lys Val Lys Glu
 50 55 60
 Leu Leu Ala Asn Pro Ala Asn Tyr Pro Ser Thr Val Thr Xaa Thr Leu
 65 70 75 80
 Ser Cys Thr Ser Val Lys Thr Met Asn Arg Trp Ala Ser Cys Pro Ala
 85 90 95
 Gly Met Thr Ala Thr Gly Cys Ala Cys Gly Phe Ala Cys Gly Ser Trp
 100 105 110
 Glu Ile Gln Ser Gly Xaa Thr Cys Asn Cys Leu Cys Leu Leu Leu Thr

115

120

125

Gly Ser

130

<210> 133

<211> 455

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (409)

<223> N = A, C, G OR T/U

<400> 133

```

gaattcgcgg cgcgcgcgac ggaaagggtca agctgggttcc aaatactaaa atacagatgt 60
catattcggg aaaatggaaa aaatcgggatg taaaatttga agatcgattc gataaatatc 120
ttgatccatc ctttttttcag cataggattc actgggttttc aattttttaat tccttcatga 180
tggtgatctt cttagtggga ttagtttcaa tgattttaat gagaacttta aggaaagatt 240
atgcccgata cagtaaagaa gaagaaatgg atgacatgga cagagaccta ggagacgagt 300
atggctggaa gcaggtgcat ggagatgtgt tcagaccgtc aagtcaccct ctgatcttct 360
cctccctcat tggctctgga tgtcagatat ttgctgtgtc tctcattgnt attattgttg 420
ccatgataga ggacttatat acagagatgg gatcc 455

```

<210> 134

<211> 455

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (409)

<223> N = A, C, G OR T/U

<400> 134

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gaattcgcgg cgcgcgcgac ggaaagggtca agctgggttcc aaatactaaa atacagatgt 60
catattcggg aaaatggaaa aaatcgggatg taaaatttga agatcgattc gataaatatc 120
ttgatccatc ctttttttcag cataggattc actgggttttc aattttttaat tccttcatga 180
tggtgatctt cttagtggga ttagtttcaa tgattttaat gagaacttta aggaaagatt 240
atgcccgata cagtaaagaa gaagaaatgg atgacatgga cagagaccta ggagacgagt 300
atggctggaa gcaggtgcat ggagatgtgt tcagaccgtc aagtcaccct ctgatcttct 360
cctccctcat tggctctgga tgtcagatat ttgctgtgtc tctcattgnt attattgttg 420
ccatgataga ggacttatat acagagatgg gatcc 455

```

<210> 135

<211> 151

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (136)
<223> XAA = ANYTHING

<400> 135

Ile Arg Gly Arg Val Asp Gly Lys Val Lys Leu Val Pro Asn Thr Lys
1 5 10 15

Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe
20 25 30

Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg
35 40 45

Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu
50 55 60

Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr
65 70 75 80

Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu
85 90 95

Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro
100 105 110

Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln
115 120 125

Ile Phe Ala Val Ser Leu Ile Xaa Ile Ile Val Ala Met Ile Glu Asp
130 135 140

Leu Tyr Thr Glu Met Gly Ser
145 150

<210> 136
<211> 490
<212> DNA
<213> Mus musculus

<400> 136

gaattcgagg ccgcgtcgac ccaaattccat cactgtcttc tttaaagaga tagaagttat 60
attcagtgca acgaccagtg aagtatcatg gatatcatct ataatggttg ctgtcatgta 120
tgctggagggt cctatcagca gtatcttgggt gaataaatac ggcagccgtc cagtaatgat 180
cgctgggtggg tgtctgtctg gttgcggctt gatcgagct tctttctgta acacagtaca 240
ggaacttttac ttgtgcattg gtgttattgg aggtcttggg cttgctttca acttgaaccc 300
agctctgact atgattggca agtattttcta caagaagcga ccactggcca acggactggc 360
catggcaggc agccctgtgt tcctctctac cctggctcca cttaatcagg ctttctttga 420
tatttttgac tggagaggaa gcttcctaata tcttgggggc ctctcctaa attgttgtgt 480
agctggatcc 490

<210> 137
<211> 163
<212> PRT

<213> Mus musculus

<400> 137

Asn Ser Arg Pro Arg Arg Pro Lys Ser Ile Thr Val Phe Phe Lys Glu
1 5 10 15
Ile Glu Val Ile Phe Ser Ala Thr Thr Ser Glu Val Ser Trp Ile Ser
20 25 30
Ser Ile Met Leu Ala Val Met Tyr Ala Gly Gly Pro Ile Ser Ser Ile
35 40 45
Leu Val Asn Lys Tyr Gly Ser Arg Pro Val Met Ile Ala Gly Gly Cys
50 55 60
Leu Ser Gly Cys Gly Leu Ile Ala Ala Ser Phe Cys Asn Thr Val Gln
65 70 75 80
Glu Leu Tyr Leu Cys Ile Gly Val Ile Gly Gly Leu Gly Leu Ala Phe
85 90 95
Asn Leu Asn Pro Ala Leu Thr Met Ile Gly Lys Tyr Phe Tyr Lys Lys
100 105 110
Arg Pro Leu Ala Asn Gly Leu Ala Met Ala Gly Ser Pro Val Phe Leu
115 120 125
Ser Thr Leu Ala Pro Leu Asn Gln Ala Phe Phe Asp Ile Phe Asp Trp
130 135 140
Arg Gly Ser Phe Leu Ile Leu Gly Gly Leu Leu Leu Asn Cys Cys Val
145 150 155 160
Ala Gly Ser

<210> 138

<211> 358

<212> DNA

<213> Mus musculus

<400> 138

gaattcgagg cgcgtttnga cgcggcggcg ggcggcgcgc tggatgatcg ctggtgcatc 60
ttcggcctct tgctcctggc tatattggcc ttttgctggg tctacgttcg gaagtaccag 120
agtcagcggg aaagtgaggt cgtctccact gtgacagcca ttttttcact ggctgttgct 180
ctgatcacat cagcactgct gcgggtggat atatttttgg tttcttacat gaaaaatcaa 240
aatggcacat tcaaggactg ggctgacgcc aatgtcaccg tacagattga gaataccggt 300
ctgtatggct actatactct gtattctgtc attctcttct gtgtgttctt ctggatcc 358

<210> 139

<211> 356

<212> DNA

<213> Mus musculus

<400> 139

gaattcgcgg ccgcgtcgac gttttttggt ttttgttttt gtgtttgttt ttgttttttt 60
gagccagggc aatacagaaa aaaaacaaac aaacaaacaa aatgtagtgt aaagtggcct 120
gtggttctgc tgttaaagac aggttctttc atatttctca gtctagaagt cagcagtgt 180
attgtgataa tttcatattt ggaaacctaa gtgaaacttg gtgcatgata tttattcttc 240
aaaatgcagg taagctgatg gccatatctg tctggatatg gtttgttctt tagactgagc 300
ctctgtggtt tgctaactgg gtacatgttt tattgacagc aatatgttta ggatcc 356

<210> 140

<211> 115

<212> PRT

<213> Mus musculus

<400> 140

Ile Arg Gly Arg Val Asp Val Phe Cys Phe Leu Phe Leu Cys Leu Phe
1 5 10 15

Leu Phe Phe Ala Arg Ala Ile Gln Lys Lys Asn Lys Gln Thr Asn Lys
20 25 30

Met Cys Lys Val Ala Cys Gly Ser Ala Val Lys Asp Arg Phe Phe His
35 40 45

Ile Ser Gln Ser Arg Ser Gln Gln Cys Asn Cys Asp Asn Phe Ile Phe
50 55 60

Gly Asn Leu Ser Glu Thr Trp Cys Met Ile Phe Ile Leu Gln Asn Ala
65 70 75 80

Gly Lys Leu Met Ala Ile Ser Val Trp Ile Trp Phe Val Leu Thr Glu
85 90 95

Pro Leu Trp Phe Ala Asn Trp Val His Val Leu Leu Thr Ala Ile Cys
100 105 110

Leu Gly Ser
115

<210> 141

<211> 300

<212> DNA

<213> Mus musculus

<400> 141

gaattcgcgg ccgcgtcgac ggacacttaa gagaagtata ttaaactctga tcttgctatg 60
tatcttttta aaatatagta ttaacatact aatataatgc taattgaaaa attaaagtac 120
atatttttgt gtacatgtgt gtgcatatac gcgtgtgccca tgggtgtgcgt gtggagagca 180
ggggacagct tgccatagct ggctctctac tgccatgaca tgggtcttag ggatcgagtt 240
catgccacta ggcttcatgt tacgggtctt cctggccctg taaatatttt gaagggatcc 300

<210> 142

<211> 96
 <212> PRT
 <213> Mus musculus

<400> 142
 Glu Phe Ala Ala Ala Ser Thr Asp Thr Glu Lys Tyr Ile Lys Ser Asp
 1 5 10 15
 Leu Ala Met Tyr Leu Phe Lys Ile Tyr His Thr Asn Ile Met Leu Ile
 20 25 30
 Glu Lys Leu Lys Tyr Ile Tyr Leu Cys Thr Cys Val Cys Ile Tyr Ala
 35 40 45
 Cys Ala Met Val Cys Val Trp Arg Ala Gly Asp Ser Leu Pro Leu Ala
 50 55 60
 Leu Tyr Cys His Asp Met Gly Leu Arg Asp Arg Val His Ala Thr Arg
 65 70 75 80
 Leu His Val Thr Gly Leu Pro Gly Pro Val Asn Ile Leu Lys Gly Ser
 85 90 95

<210> 143
 <211> 897
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (580)..(896)
 <223> N = A, C, G OR T/U

<400> 143
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 atgtaggggt cagtgatgtg cagtcgcttg tggacttaac taagtttaa ttaaaaaaat 120
 gatttttttt gtttttttaa attaaaagac attattttgt gtgagggggg agaagagtg 180
 tgagggttaga gccccataga tactaaacta gaagtcttgt ttataatagg ttgacactgg 240
 caagttgtta atctctcagt ggtagtcttt ctatctctaa agtgggtataa gtattgatgc 300
 ttgtgttgag agtatttgct aggattagaa atcattggaa ataatgaatc aagataaaaa 360
 atggcactgg aggtaggaag ctgagggcat agaatgtcac ggttctggga agttagttgg 420
 aagctgagaa gttggtgata ttctggattt gctatactcg attttatctg cccatctctt 480
 gattgacact ggcatacttg gcatatagac ttccaagaaa agatgttagc tattatggaa 540
 ggagcattgt gtagagaccc tggagaaagg ggtagctctn caagtaggtt ctcaattaac 600
 ataggtagag cggcgggtga cggccactgt gaactctttc ctatctactt attggtcctt 660
 tagctctcac ctacttcta ctttccttaa cccgagcacc caggagtctg ntcttcaact 720
 cttgagagaa gtaaaagatg gcttatgaaa antttantag ctgcacatag gaatgaagg 780
 gtgggctntg gaccngatga tgganattga atccctggcc ttactactat gggatttngg 840
 taattaaatg gcttggaac tgaaataatt ggggggtatg aggatanttt ganannt 897

<210> 144
 <211> 357
 <212> DNA
 <213> Mus musculus

<400> 144
 gaattcgcgg ccgcgtcgac gcggcggcgg cggccgagct ggtgatcggc tgggtgcatct 60
 tcggcctctt gtcctggct attttggcct tttgctgggt ctacgttcgg aagtaccaga 120
 gtcagcggga aagtgaggtc gtctccactg tgacagccat tttttcactg gctgttgctc 180
 tgatcacatc agcactgctg ccggtggata tatttttggg ttcttacatg aaaaatcaaa 240
 atggcacatt caaggactgg gctgacgcca atgtcaccgt acagattgag aataccgttc 300
 tgtatggcta ctatactctg tattctgtca ttctcttctg tgtgttcttc tggatcc 357

<210> 145
 <211> 115
 <212> PRT
 <213> Mus musculus

<400> 145
 Glu Phe Ala Ala Ala Ser Thr Arg Arg Arg Arg Pro Ser Trp Ser Ala
 1 5 10 15
 Gly Ala Ser Ser Ala Ser Cys Ser Trp Leu Phe Trp Pro Phe Ala Gly
 20 25 30
 Ser Thr Phe Gly Ser Thr Arg Val Ser Gly Lys Val Arg Ser Ser Pro
 35 40 45
 Leu Gln Pro Phe Phe His Trp Leu Leu Leu Ser His Gln His Cys Cys
 50 55 60
 Arg Trp Ile Tyr Phe Trp Phe Leu Thr Lys Ile Lys Met Ala His Ser
 65 70 75 80
 Arg Thr Gly Leu Thr Pro Met Ser Pro Tyr Arg Leu Arg Ile Pro Phe
 85 90 95
 Cys Met Ala Thr Ile Leu Cys Ile Leu Ser Phe Ser Ser Val Cys Ser
 100 105 110
 Ser Gly Ser
 115

<210> 146
 <211> 346
 <212> DNA
 <213> Mus musculus

<400> 146
 gaattcgcgg ccgcgtcgac ctataatctg tctacctatc taaccaccat acatctatct 60
 catctatata ttcacttata cacctattta agtatctatt gacctatgta gctactatgt 120
 atctacccat gtgtctacct gtgtgtctat ttatcacata tctgtctgtc tgtctgtcta 180
 tcatttgcct atctacttat ttacttagga aacaaacatg gagatgtttt tgttcaagt 240

caaggatttt ataaaagcat ctataaaaaat ctgtgtcatg gtctttgtcc tcattgatat 300
aggactgttt agtaccagca cctgctatac tctagccact ggatcc 346

<210> 147
<211> 112
<212> PRT
<213> Mus musculus

<400> 147
Asn Ser Arg Pro Arg Arg Pro Ile Ile Cys Leu Pro Ile Pro Pro Tyr
1 5 10 15
Ile Tyr Leu Ile Tyr Ile Phe Ile Tyr Thr Pro Ile Val Ser Ile Asp
20 25 30
Leu Cys Ser Tyr Tyr Val Ser Thr His Val Ser Thr Cys Val Ser Ile
35 40 45
Tyr His Ile Ser Val Cys Leu Ser Val Tyr His Leu Pro Ile Tyr Leu
50 55 60
Phe Thr Glu Thr Asn Met Glu Met Phe Leu Phe Lys Cys Lys Asp Phe
65 70 75 80
Ile Lys Ala Ser Ile Lys Ile Cys Val Met Val Phe Val Leu Ile Asp
85 90 95
Ile Gly Leu Phe Ser Thr Ser Thr Cys Tyr Thr Leu Ala Thr Gly Ser
100 105 110

<210> 148
<211> 962
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (672)..(961)
<223> N = A, C, G OR T/U

<400> 148
gaattcgagg ccgcgtcgac gtagactggt tggcttggtt caaggattca gcaaattctct 60
gcaagttagt gctttgcatg gtgcctggcc catggtaaataaatgtcctg gcaagttaaa 120
gtcttcagag ctctatatac atttgaacct agaactccag atgaattata ctttgaagaa 180
ggagacatta tctacatcac tgacatgagt gataccagct ggtggaaagg gacatgcaag 240
ggcagaacag gactgatccc gagcaactat gtggctgagc aggcagaatc cattgacaat 300
ccattgcatg aagctgcaaa aagaggcaac ctgagctggt tgagggagtg cttggacaac 360
cggggtgggtg tgaacggcct ggacaaagct ggaagcacag ccctgtactg ggcttgccac 420
ggtggccata aagacatagt ggaggttctg tttactcagc ccgaatgtgg agctgaacca 480
gcagaataag ctgggagaca cagctctgca cgcggctgcc tgggaagggtt atgcagacat 540

tgtccagttg ctactggcaa aagggtgagac gacagacttg agaaacaatg agaagaagct 600
gccttggaca tggccaccaa cgctgcctgt gcatcgcttc tgaagaagaa gcagcagggg 660
acagatgggg cntcgaacgt taagcaacgc ccgaaggact tancttcgat gaccaaagac 720
ntcagactgg attccccccg ggggccgggtt ttgaatgggtt ggccataaact ttcttttngc 780
ttttngncaa tttccgggaa ccttnggggtt ggnttngncc cnaaaaaagt nnttggataa 840
ccnggtggcn tttttaaag gtctgggatt gaaaccccga anacttgggtt ggcacttggg 900
ggattcccaa cccagaaaa acccttgggtg naaaggtaaa aagnnagnct tgaaaaatcc 960
nt 962

<210> 149
<211> 296
<212> DNA
<213> Mus musculus

<400> 149
gaattcgagg ccgcgctcga cttttttttt tttttgactg tcctaaattg tttattggat 60
atgaatttta caaatatcac gtgtattagc ggtaacgggtg gagctggaga gtattgcgcc 120
ttctccaggc tgcacggcgg gaaccaccaa tagtgtgggtg gaacttgggtg ccctttccaa 180
ggccacgggt ctttcggcca gcagatgtca gccacgcat ctctctgtgt ttgtggactg 240
gtttgggtgat ccactgggtg tcaggatttc ttctgatagc tttatggaac ggatcc 296

<210> 150
<211> 67
<212> PRT
<213> Mus musculus

<400> 150
Arg Trp Ser Trp Arg Val Leu Arg Leu Leu Gln Ala Ala Arg Arg Glu
1 5 10 15
Pro Pro Ile Val Trp Trp Asn Leu Trp Pro Phe Pro Arg Pro Arg Leu
20 25 30
Phe Arg Pro Ala Asp Val Ser Pro Arg Ile Ser Leu Cys Leu Trp Thr
35 40 45
Gly Leu Val Ile His Trp Val Ser Gly Phe Leu Leu Ile Ala Leu Trp
50 55 60
Asn Gly Ser
65

<210> 151
<211> 356
<212> DNA
<213> Mus musculus

<400> 151
gaattcgagg ccgcgctcga gttttttgtt ttttgtttt gtgtttgttt ttgttttttt 60
gagccagggc aatacagaaa aaaaacaaac aaacaaacaa aatgtagtgt aaagtggcct 120
gtggttctgc tgtaaagac aggttctttc atatttctca gtctagaagt cagcagtgt 180
attgtgataa tttcatattt ggaaacctaa gtgaaacttg gtgcatgata tttattcttc 240

aaaatgcagg taagctgatg gccatatctg tctggatatg gtttgttctt tagactgagc 300
ctctgtgggt tgctaactgg gtacatgttt tattgacagc aatatgttta ggatcc 356

<210> 152
<211> 669
<212> DNA
<213> Mus musculus

<400> 152
gaattcgagg cccgcgtcga cctctctgtg aggagtgcag aaacatagtg ttcaaaatgc 60
ctgctgaaat gcaagcccct cagtggctcc tgctgctact gggtatcctg ccagccacag 120
gctcagaccc tgtgctctgc ttcacccagt atgaggagtc ctctggcagg tgcaaaggcc 180
tacttggggag agacatcagg gtagaagact gctgtctcaa cgctgcctat gccttccagg 240
agcatgatgg tggcctctgt caggcatgca ggtctccaca atggtcagca tggtccttat 300
ggggggccctg ctcatgtaca tgttctgagg ggtcccagct gcgacacagg cgctgtgtgg 360
gcagagggtgg tcagtgtctc gagaatgtgg ctccctggaac tcttgagtgg cagctacagg 420
cctgtgagga ccagccatgc tgtccagaga tgggtggctg gtctgagtgg ggaccctggg 480
ggccttgctc tgtcacatgc tccaaaggaa ccagatccg tcaacgagta tgtgataatc 540
ctgtctcctaa gtgtgggggc cactgcccag gaagaggccc agcaatcaca ggccttgtga 600
caccagaag acctgcccga cacatggggc tgggcatcct ggggcccctg gagcccttgt 660
tcaggatcc 669

<210> 153
<211> 220
<212> PRT
<213> Mus musculus

<400> 153
Glu Phe Ala Ala Arg Val Asp Leu Ser Val Arg Ser Ala Glu Thr Cys
1 5 10 15
Ser Lys Cys Leu Leu Lys Cys Lys Pro Leu Ser Gly Ser Cys Cys Tyr
20 25 30
Trp Leu Ser Cys Gln Pro Gln Ala Gln Thr Leu Cys Ser Ala Ser Pro
35 40 45
Ser Met Arg Ser Pro Leu Ala Gly Ala Lys Ala Tyr Leu Gly Glu Thr
50 55 60
Ser Gly Lys Thr Ala Val Ser Thr Leu Pro Met Pro Ser Arg Ser Met
65 70 75 80
Met Val Ala Ser Val Arg His Ala Gly Leu His Asn Gly Gln His Gly
85 90 95
Pro Tyr Gly Gly Pro Ala Gln Leu His Val Leu Arg Gly Pro Ser Cys
100 105 110
Asp Thr Gly Ala Val Trp Ala Glu Val Val Ser Ala Leu Arg Met Trp
115 120 125
Leu Leu Glu Leu Leu Ser Gly Ser Tyr Arg Pro Val Arg Thr Ser His

130 135 140

Ala Val Gln Arg Trp Val Ala Gly Leu Ser Gly Asp Pro Gly Gly Leu
 145 150 155 160

Ala Leu Ser His Ala Pro Lys Glu Pro Arg Ser Val Asn Glu Tyr Val
 165 170 175

Ile Ile Leu Leu Leu Ser Val Gly Ala Thr Ala Gln Glu Glu Ala Gln
 180 185 190

Gln Ser Gln Ala Leu His Pro Glu Asp Leu Pro His Thr Trp Ala Trp
 195 200 205

Ala Ser Trp Gly Pro Trp Ser Pro Cys Ser Gly Ser
 210 215 220

<210> 154
 <211> 179
 <212> DNA
 <213> Mus musculus

<400> 154
 gaattcgggc ccgcgggcac ttctcttgtt ggaatgttta aaaagtttagc ctactaaaga 60
 aaacagtcga cttcttgtga aggttttgga gaaatatgta tcagttcggt ttatttgggt 120
 attcaataat atccttggtg ataatgctga ctccatggct tctgatccca caaggatcc 179

<210> 155
 <211> 33
 <212> PRT
 <213> Mus musculus

<400> 155
 Arg Phe Trp Arg Asn Met Tyr Gln Phe Val Leu Phe Gly Tyr Ser Ile
 1 5 10 15

Ile Ser Leu Val Ile Met Leu Thr Pro Trp Leu Leu Ile Pro Gln Gly
 20 25 30

Ser

<210> 156
 <211> 889
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (1)..(203)
 <223> N = A, C, G OR T/U

<400> 156

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ngggggggccg ttccggncan angttggctc ccgttatatt gtnaaaactt ggggcgaatg 60
gcttgccggtt cctcngcgtt acggatngcc gttcccgatt gcagggctng cttcatngc 120
ntcctgcgag tcttctgatt gaaaaggag agtaagctga tttcccatgg ccaagnccac 180
ttctgtacct ggggtggctt cntgggttc ctgctgtcca ggcatttctg cttccagcaa 240
ggcagcccaa aggcaggtat gtcaagtggg atgccagagt cctcgggtga agagtgactt 300
gtcctagcct cctcctcctc ttgctgtca gcctagtggg ccagctagca aggaagtcca 360
ttgctgcttc tctctgacgc agacaccacc cactgtctgg agtgaagccg cctgcctttt 420
cttcctagag cactgggttct caacaccctt tgggcgtcct atatccgata tcctgcatat 480
ccaatatatta catgacgatt cacaacaggc gcaaaattac aggtatgaag tagcaacaaa 540
ataacttttag ggttggggat caccacgaca tgaggaacca tgtaaagag tctcagcgat 600
aggcaggttg agaggcgcca tcttagagct atgaccagtc agcgagggcc ttgcatacct 660
ccccgcaaaa ggaagctcag ctcaaggagt ggaatattca aagaatttgg ctttttgagt 720
agtttagctt atcctgccat tagcagaaaa tattgactgg aggggtggat tcattctaca 780
tgttttaatt ttgaaaagta tctgtattgt gagcatatgt gtgtatcttt ggatgatttg 840
tgcgatatgat tgctgggtgcc cacagagacc agcagagggc aatggatcc 889
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<210> 157

<211> 54

<212> PRT

<213> Mus musculus

<400> 157

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Leu Ile Leu Pro Leu Ala Glu Asn Ile Asp Trp Arg Gly Gly Phe Ile
  1             5             10             15
```

```
Leu His Val Leu Ile Leu Lys Ser Ile Cys Ile Val Ser Ile Cys Val
      20             25             30
```

```
Tyr Leu Trp Met Ile Cys Ala Tyr Asp Cys Trp Cys Pro Gln Arg Pro
    35             40             45
```

```
Ala Glu Gly Asn Gly Ser
    50
```

<210> 158

<211> 179

<212> DNA

<213> Mus musculus

<400> 158

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gaattcaaaa aggaagagta agcttgaatt cgggacagcg gggagtcttg aggcgcaatg 60
gatggttttg cttttatttg tgtttgataa ccatagtcgg ttatggcgac tgctatggag 120
atgtaggcaa ggcagcctcc tgtgtgacat tcaactgtaaa ccctggagat gctggatcc 179
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<210> 159

<211> 59

<212> PRT

<213> Mus musculus

<400> 159

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Ile Gln Lys Gly Arg Val Ser Leu Asn Ser Gly Gln Arg Gly Val Leu
```

1 5 10 15
 Arg Arg Asn Gly Trp Phe Cys Phe Tyr Leu Cys Leu Ile Thr Ile Val
 20 25 30
 Gly Tyr Gly Asp Cys Tyr Gly Asp Val Gly Lys Ala Ala Ser Cys Val
 35 40 45
 Thr Phe Thr Val Asn Pro Gly Asp Ala Gly Ser
 50 55

<210> 160
 <211> 215
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (9)..(27)
 <223> N = A, C, G OR T/U

<400> 160
 tgcttcncnc caagctttcc aggtgagaga taagggnac tcttggagtc aactttcacg 60
 ggtcttgatt taaaaaggaa tcacagggtcc catatccatt acttttccta ttgttgagaa 120
 caattttttt tcttttgaag atttatattat ttattttatg tgtatgcata cactatagct 180
 atcttcagac tcaccagaag agggcacttg gatcc 215

<210> 161
 <211> 69
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (2)..(11)
 <223> XAA = ANYTHING

<400> 161
 Leu Xaa Xaa Lys Leu Ser Arg Glu Ile Arg Xaa Thr Leu Gly Val Asn
 1 5 10 15
 Phe His Gly Ser Phe Lys Lys Glu Ser Gln Val Pro Tyr Pro Leu Leu
 20 25 30
 Phe Leu Leu Leu Arg Thr Ile Phe Phe Leu Leu Lys Ile Tyr Leu Phe
 35 40 45
 Ile Leu Cys Val Cys Ile His Tyr Ser Tyr Leu Gln Thr His Gln Lys
 50 55 60
 Arg Ala Leu Gly Ser
 65

<210> 162
 <211> 110
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (21)
 <223> N = A, C, G OR T/U

<400> 162
 aggagcccag gagaatctga ncaatgagga aaaagatcat aaccatattt aagacattaa 60
 acaaacaaat aattgtcttt atgcaaatag taacatcgcc agctggatcc 110

<210> 163
 <211> 34
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (28)
 <223> XAA = ANYTHING

<400> 163
 Ala Gly Asp Val Thr Ile Cys Ile Lys Thr Ile Ile Cys Leu Phe Asn
 1 5 10 15
 Val Leu Asn Met Val Met Ile Phe Phe Leu Ile Xaa Gln Ile Leu Leu
 20 25 30
 Gly Ser

<210> 164
 <211> 311
 <212> DNA
 <213> Mus musculus

<400> 164
 gaattcaggc ccgcgggggtt catgtaagtg aaggtggagt agagccctga gccctggccg 60
 gctgcgtgac tgtagtagga gccggagttc tgatggtcag cgtagtcgta ttgcgagcgg 120
 gtgatgggagc ggtaggaggg gctgtagtga ggaagggtga aggggctgta ggagatctgt 180
 tgcggggagt gctgctgctg ctgcgtgtag tggctggggc tcagctgctc cgtcttgatg 240
 tgcgttcgct gggactggcc tggctcgctg ctcagcgtgg tgagcgtgtg tgcttgctac 300
 tgtcaggatc c 311

<210> 165
 <211> 102
 <212> PRT
 <213> Mus musculus

<400> 165

Ile Gln Ala Arg Gly Val His Val Ser Glu Gly Gly Val Glu Pro Ala
1 5 10 15

Leu Ala Gly Cys Val Thr Val Val Gly Ala Gly Val Leu Met Val Ser
20 25 30

Val Val Val Leu Arg Ala Gly Asp Gly Arg Val Gly Gly Ala Val Val
35 40 45

Arg Lys Val Glu Gly Ala Val Gly Asp Leu Leu Arg Gly Val Leu Leu
50 55 60

Leu Leu Ala Val Val Ala Gly Ala Gln Leu Leu Arg Leu Asp Val Arg
65 70 75 80

Ser Leu Gly Leu Ala Trp Leu Ala Ala Gln Arg Gly Glu Arg Val Cys
85 90 95

Leu Leu Leu Ser Gly Ser
100

<210> 166

<211> 113

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (1)..(24)

<223> XAA = ANYTHING

<400> 166

Xaa Val Ser Xaa Asn Ser Gly Xaa Xaa Arg Gly Val Xaa Leu Gly Leu
1 5 10 15

Arg Ser Val Ala Xaa Gly Phe Xaa Asp Thr Glu Val Thr Thr Pro Met
20 25 30

Gly Thr Ala Glu Val Ala Pro Asp Thr Ser Pro Arg Ser Gly Pro Ser
35 40 45

Cys Trp His Arg Leu Val Gln Val Phe Gln Ser Lys Gln Phe Arg Ser
50 55 60

Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe Phe Gln Met Asn Gln
65 70 75 80

Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val Leu Leu Met Ala Val
85 90 95

Leu Leu Thr Phe His Ala Ala Pro Ala Gln Pro Gln Pro Ala Tyr Gly
100 105 110

Ser

<210> 167
<211> 248
<212> DNA
<213> Mus musculus

<400> 167
acatctctcg gaggaccatg ggctctggcg ggaagagagc cttcgagagg cggtagagat 60
tgcgaagggt gaactggatg ctggtgttgg tgacgcgaag ctcgaggatg ttggtggagc 120
tgtcctgagg gcagatgtca ctctgcctg agaatgggga cactgtgatg gtattcttca 180
gctcataaag tggcaagttg tctgaaatgc cgccatccac atagcgcacc ccttagaggc 240
taggatcc 248

<210> 168
<211> 107
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (2)..(30)
<223> XAA = ANYTHING

<400> 168
Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Ser Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Leu Xaa Cys Xaa Xaa Ile Ser
20 25 30
Arg Arg Thr Met Gly Ser Gly Gly Lys Arg Ala Phe Glu Arg Arg Arg
35 40 45
Leu Arg Arg Leu Asn Trp Met Leu Val Leu Val Thr Arg Ser Ser Trp
50 55 60
Met Leu Val Glu Leu Ser Gly Gln Met Ser Leu Ser Pro Glu Asn Gly
65 70 75 80
Asp Thr Val Met Val Phe Phe Ser Ser Ser Gly Lys Leu Ser Glu Met
85 90 95
Pro Pro Ser Thr Arg Thr Pro Arg Leu Gly Ser
100 105

<210> 169
<211> 420
<212> DNA
<213> Mus musculus

<220>
 <221> modified_base
 <222> (46)..(63)
 <223> N = A, C, G OR T/U

<400> 169
 gaattcgcgg ccgcgtcgac cttttttttt tttttttttt ttttntttt tttttntn 60
 nnnnggatttt tccaagataa aactttattg gagacagcaa ggagtatact gaaagtgggg 120
 gagccatgcc ttcattccat aactgcaatc agatgctctc ctctgagaga gagtgtgtgg 180
 ggagccaagg tgagaagcag gtatgattca caccccaact gcttggagag tgcttatatg 240
 acagtctttt tctcgatttt attttttctc agttcttcaa cacacacttt ggcttcattt 300
 ggggggaaaat taaacaaaag aacagaattt ccttccccca gagttactta tgaaatgaca 360
 cagctgcctt tttctttgaa gggattcttg tcttctggga ttccctttac cagaggatcc 420

<210> 170
 <211> 140
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (16)..(21)
 <223> XAA = ANYTHING

<400> 170
 Glu Phe Ala Ala Ala Ser Thr Phe Phe Phe Phe Phe Phe Phe Phe Xaa
 1 5 10 15
 Phe Phe Phe Xaa Xaa Gly Phe Phe Gln Asp Lys Thr Leu Leu Glu Thr
 20 25 30
 Ala Arg Ser Ile Leu Lys Val Gly Glu Pro Cys Leu His Ser Ile Thr
 35 40 45
 Ala Ile Arg Cys Ser Pro Leu Arg Glu Ser Val Trp Gly Ala Lys Val
 50 55 60
 Arg Ser Arg Tyr Asp Ser His Pro Asn Cys Leu Glu Ser Ala Tyr Met
 65 70 75 80
 Thr Val Phe Phe Ser Ile Leu Phe Phe Leu Ser Ser Ser Thr His Thr
 85 90 95
 Leu Ala Ser Phe Gly Gly Lys Leu Asn Lys Arg Thr Glu Phe Pro Ser
 100 105 110
 Pro Arg Val Thr Tyr Glu Met Thr Gln Leu Pro Phe Ser Leu Lys Gly
 115 120 125
 Phe Leu Ser Ser Gly Ile Pro Phe Thr Arg Gly Ser
 130 135 140

<210> 171
 <211> 334
 <212> DNA
 <213> Mus musculus

<400> 171
 gaattcgcgg ccgcgtcgac ggcggctccg gaggtgctgg agtcagacgt gtcaagttcg 60
 ataacacttt tgaaaaacct ccaggagcag gtgagtatgt atgtctttta gaataaatca 120
 gtcagggggtt aactttgact ttgtaagtct catccacaca ctttgatgat tcgaataacta 180
 caaaaattatc ttaggtgtaa aataaaagcc ttatatgcgc ttcattgaaag ttcaaaataa 240
 ttcattcagc tcccaaagaa atacagaaag ctgtttttcc cccattcact tacttattta 300
 tttattttat ttagtcactt tacattccgg atcc 334

<210> 172
 <211> 105
 <212> PRT
 <213> Mus musculus

<400> 172
 Asn Ser Arg Pro Arg Arg Arg Arg Leu Arg Arg Cys Trp Ser Gln Thr
 1 5 10 15
 Cys Gln Val Arg His Phe Lys Thr Ser Arg Ser Arg Val Cys Met Ser
 20 25 30
 Phe Arg Ile Asn Gln Ser Gly Val Asn Phe Asp Phe Val Ser Leu Ile
 35 40 45
 His Thr Leu Phe Glu Tyr Tyr Lys Ile Ile Leu Gly Val Lys Lys Pro
 50 55 60
 Tyr Met Arg Phe Met Lys Val Gln Asn Asn Ser Phe Ser Ser Gln Arg
 65 70 75 80
 Asn Thr Glu Ser Cys Phe Ser Pro Ile His Leu Leu Ile Tyr Leu Phe
 85 90 95
 Tyr Leu Val Thr Leu His Ser Gly Ser
 100 105

<210> 173
 <211> 648
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (11) .. (43)
 <223> N = A, C, G OR T/U

<400> 173
 tccacagtac ntgcctntaga agccttggac ctgcengtcc tcntaggcca cttcaggctc 60
 agatgctacc aatgttgtct ccttgaacag agtctgagcc ccctgccagc tccttcttcc 120


```

atttcctagg agcattgtgg gtgtgccagt ggatggctgg ctgacgtgtg gatagactga 180
tggtgtgtgt ctagatgggt gtggtgggtg tatggatgat ggatggatgg gtgggtgggt 240
gaatggatga atggatgagt ggggtggtagg tatgtaattg ggtaaataat ggatagatac 300
atatttaggg agaaatcttt ttctagagag tttgtttaaa aactagccaa gcttaggtgg 360
caaccggaac aaagatgggt ccaagtgtag ggaggggtct gatgccttcc acgtggtttt 420
agctcttatt ttatgattga ttgttcagta attcctgcat taaccaagtg gagactgact 480
ttggaacaat ctaagtggat tatttttagcg ggcttccctt tggtgggggt catgctggct 540
caggtgtgga ttaaccacag tcacttcctc tcagccttgc tggactgtgg tggacgggat 600
cttagcaggg tgaaggcagc ccagatgatg agagaggcga ggggatcc 648

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```

<210> 174
<211> 208
<212> PRT
<213> Mus musculus

```

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<220>
<221> MOD_RES
<222> (4)..(15)
<223> XAA = ANYTHING

```

```

<400> 174
Ser Thr Val Xaa Ala Xaa Glu Ala Leu Asp Leu Pro Val Leu Xaa Gly
  1              5              10              15
His Phe Arg Leu Arg Cys Tyr Gln Cys Cys Leu Leu Glu Gln Ser Leu
      20              25              30
Ser Pro Leu Pro Ala Pro Ser Ser Ile Ser Glu His Cys Gly Cys Ala
      35              40              45
Ser Gly Trp Leu Ala Asp Val Trp Ile Asp Trp Cys Val Ser Arg Trp
      50              55              60
Trp Trp Trp Val Tyr Gly Trp Met Asp Gly Trp Val Gly Glu Trp Met
      65              70              75              80
Asn Gly Val Gly Gly Arg Tyr Val Ile Gly Met Met Asp Arg Tyr Ile
      85              90              95
Phe Arg Glu Lys Ser Phe Ser Arg Glu Phe Val Lys Leu Ala Lys Leu
      100             105             110
Arg Trp Gln Pro Glu Gln Arg Trp Ser Gln Val Gly Gly Val Cys Leu
      115             120             125
Pro Arg Gly Phe Ser Ser Tyr Phe Met Ile Asp Cys Ser Val Ile Pro
      130             135             140
Ala Leu Thr Lys Trp Arg Leu Thr Leu Glu Gln Ser Lys Trp Ile Ile
      145             150             155             160
Leu Ala Gly Phe Pro Leu Ala Gly Val Met Leu Ala Gln Val Trp Ile
      165             170             175

```

Asn His Ser His Phe Leu Ser Ala Leu Leu Asp Cys Gly Gly Arg Asp
 180 185 190

Leu Ser Arg Val Lys Ala Ala Gln Met Met Arg Glu Ala Arg Gly Ser
 195 200 205

<210> 175
 <211> 619
 <212> DNA
 <213> Mus musculus

<400> 175
 gaagtgaaag ttcgtccaag gcagcacaac tgcacttggtg tgttataaca gccagatcac 60
 agctccctat gcggaccgag tcaccttctc atccagtggc atcacgttca gttctgtgac 120
 ccggaaggac aatggagagt atacttgcac ggtctccgag gaaggtggcc agaactacgg 180
 ggaggtcagc atccacctca ctgtgcttgt acctccatcc aagccgacga tcagtgtccc 240
 ctctctgtgc accattggga acagggcagt gctgacctgc tcagagcatg atggttcccc 300
 accctctgaa tattcctggt tcaaggacgg gatatccatg cttacagcag atgccaagaa 360
 aacccggggc ttcattgaatt cttcattcac cattgatcca aagtcggggg atctgatctt 420
 tgaccccggtg acagcctttg atagtgggtga atactactgc caggcccaga atggatatgg 480
 gacagccatg aggtcagagg ctgcacacat ggatgctgtg gagctgaatg tggggggcat 540
 cgtggcagct gtcctggtaa cactgattct ccttggactc ttgattttttg gcgtctgggt 600
 tgcctatagc cagcatcc 619

<210> 176
 <211> 205
 <212> PRT
 <213> Mus musculus

<400> 176
 Lys Lys Phe Val Gln Gly Ser Thr Thr Ala Leu Val Cys Tyr Asn Ser
 1 5 10 15
 Gln Ile Thr Ala Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Ser Gly
 20 25 30
 Ile Thr Phe Ser Ser Val Thr Arg Lys Asp Asn Gly Glu Tyr Thr Cys
 35 40 45
 Met Val Ser Glu Glu Gly Gly Gln Asn Tyr Gly Glu Val Ser Ile His
 50 55 60
 Leu Thr Val Leu Val Pro Pro Ser Lys Pro Thr Ile Ser Val Pro Ser
 65 70 75 80
 Ser Val Thr Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu His Asp
 85 90 95
 Gly Ser Pro Pro Ser Glu Tyr Ser Trp Phe Lys Asp Gly Ile Ser Met
 100 105 110

Leu Thr Ala Asp Ala Lys Lys Thr Arg Ala Phe Met Asn Ser Ser Phe
 115 120 125

Thr Ile Asp Pro Lys Ser Gly Asp Leu Ile Phe Asp Pro Val Thr Ala
 130 135 140

Phe Asp Ser Gly Glu Tyr Tyr Cys Gln Ala Gln Asn Gly Tyr Gly Thr
 145 150 155 160

Ala Met Arg Ser Glu Ala Ala His Met Asp Ala Val Glu Leu Asn Val
 165 170 175

Gly Gly Ile Val Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Leu
 180 185 190

Leu Ile Phe Gly Val Trp Phe Ala Tyr Ser His Gly Ser
 195 200 205

<210> 177

<211> 542

<212> DNA

<213> Mus musculus

<400> 177

gaattcgcgg ccgcgtcgac caagcccaga tgttgctgag catgaacagc ctggagtcgc 60
 tgaatgcggg tgtacagcag aacaatactg agtcctttgc cgtcgctctc tgccatcttg 120
 cagagctcca tgcagaacag ggctgttttg cggctgctgg tgaagtatta aagcacttga 180
 aggaccgatt tccacccaac agtcagcacg cccagttatg gatgctgtgt gatcaaaaaa 240
 tacagtttga cagagcaatg aatgatggca aattccattt ggctgattca cttgttacag 300
 gaatcacagc gcttaatggc atagaagggtg tatacaggaa agcagtcgta ctgcaggctc 360
 agaaccaaat gacagaggca cacaagctac tacagaagtt gctgacatac tgtcagaagt 420
 taaagaacac agaaatgggtc atcagtgctc tcctatcggt ggcagagctg tactggcgat 480
 ctctgtcccc gaccatcgcc atgcctgtgc tcctggaagc tctggccctc tccaaaggat 540
 cc 542

<210> 178

<211> 180

<212> PRT

<213> Mus musculus

<400> 178

Ile Arg Gly Arg Val Asp Gln Ala Gln Met Leu Leu Ser Met Asn Ser
 1 5 10 15

Leu Glu Ser Leu Asn Ala Gly Val Gln Gln Asn Asn Thr Glu Ser Phe
 20 25 30

Ala Val Ala Leu Cys His Leu Ala Glu Leu His Ala Glu Gln Gly Cys
 35 40 45

Phe Ala Ala Ala Gly Glu Val Leu Lys His Leu Lys Asp Arg Phe Pro
 50 55 60

Pro Asn Ser Gln His Ala Gln Leu Trp Met Leu Cys Asp Gln Lys Ile
65 70 75 80

Gln Phe Asp Arg Ala Met Asn Asp Gly Lys Phe His Leu Ala Asp Ser
85 90 95

Leu Val Thr Gly Ile Thr Ala Leu Asn Gly Ile Glu Gly Val Tyr Arg
100 105 110

Lys Ala Val Val Leu Gln Ala Gln Asn Gln Met Thr Glu Ala His Lys
115 120 125

Leu Leu Gln Lys Leu Leu Thr Tyr Cys Gln Lys Leu Lys Asn Thr Glu
130 135 140

Met Val Ile Ser Val Leu Leu Ser Val Ala Glu Leu Tyr Trp Arg Ser
145 150 155 160

Ser Ser Pro Thr Ile Ala Met Pro Val Leu Leu Glu Ala Leu Ala Leu
165 170 175

Ser Lys Gly Ser
180

<210> 179

<211> 640

<212> DNA

<213> Mus musculus

<400> 179

caagtcaatg tacaaaaatgt ctggcaatgc ctcatttaaa attaaattgg tttattgaga 60
acagctgttt ttgatgtgta acgtgaagca agacagagcc ctgctgtgag cagctggcag 120
aagatttttt ttttttaatt attggtacat attacccttc aaatctgaga atttggacta 180
attgcaccaa agaaccctct aatttggtcc ctggcacatg cgtacctgtc aacttttttt 240
cttttacaag acctgcatgc tgtcggccat cgccttctcc aatgtttttg agcactattt 300
gggggatgac atgaaaaggg aaaaccacc tgtggaggac agcagtgatg aggatgacaa 360
aagaaacca ggaaacttgt atgacaaggc aggtaaagtg aggaagcatg tgacagagca 420
agagaaacct gaagagggtc tgggcccacaa catcaaaagc attgtgacca tgctgatgct 480
catgctcctg atgatgttcg cgggtccactg cactgtgggtc acaagcaacg cctactccag 540
tccaagtgtg gtccttgcct cctacaatca tgatggtacc aggaatatat tagatgattt 600
tagagaagcg tacttttggc tgagacaaaa caccgatcc 640

<210> 180

<211> 209

<212> PRT

<213> Mus musculus

<400> 180

Lys Ser Met Tyr Lys Met Ser Gly Asn Ala Ser Phe Lys Ile Lys Leu
1 5 10 15

Val Tyr Glu Gln Leu Phe Leu Met Cys Asn Val Lys Gln Asp Arg Ala

20 25 30
 Leu Leu Ala Ala Gly Arg Arg Phe Phe Phe Phe Asn Tyr Trp Tyr Ile
 35 40 45
 Leu Pro Phe Lys Ser Glu Asn Leu Asp Leu His Gln Arg Thr Leu Phe
 50 55 60
 Gly Pro Trp His Met Arg Thr Cys Gln Leu Phe Phe Phe Tyr Lys Thr
 65 70 75 80
 Cys Met Leu Ser Ala Ile Ala Phe Ser Asn Val Phe Glu His Tyr Leu
 85 90 95
 Gly Asp Asp Met Lys Arg Glu Asn Pro Pro Val Glu Asp Ser Ser Asp
 100 105 110
 Glu Asp Asp Lys Arg Asn Pro Gly Asn Leu Tyr Asp Lys Ala Gly Lys
 115 120 125
 Val Arg Lys His Val Thr Glu Gln Glu Lys Pro Glu Glu Gly Leu Gly
 130 135 140
 Pro Asn Ile Lys Ser Ile Val Thr Met Leu Met Leu Met Leu Leu Met
 145 150 155 160
 Met Phe Ala Val His Cys Thr Trp Val Thr Ser Asn Ala Tyr Ser Ser
 165 170 175
 Pro Ser Val Val Leu Ala Ser Tyr Asn His Asp Gly Thr Arg Asn Ile
 180 185 190
 Leu Asp Asp Phe Arg Glu Ala Tyr Phe Trp Leu Arg Gln Asn Thr Gly
 195 200 205

Ser

<210> 181

<211> 671

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (5)..(71)

<223> N = A, C, G OR T/U

<400> 181

agccngttta tctttgggta canaaagccc actgattggt ttgtgttatt ttatatcaag 60
 ctactgcact naagctgttt atctggttta ggagttctct ggtgaatttt agggtcactt 120
 atatatacta tcatatcatc tgcaaatagt gatatttttg acttcttctt tccaatttgt 180
 atccccttga cctccttttg ttgtggaatt gctctgggcta ggacttcaag tactatattg 240
 aataggtggg gagaaagtgg cagcttgtct agtcctgat ttagtgggga ttgcttccag 300

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tttctatcca tttactttga tgttggctac tggtttgctg tagattgctt ttattatggt 360
caggatggg ccttgaattc ctgatcttcc caagactttt atcttgaatg ggtgttggat 420
tttgtcaaat gctttttccg catctaata tcatgtgggt tttgtctttg agtttgcttt 480
tatagtggat tacaatgatg gatttccgta tattaaacca tccctgcac cctgggatga 540
agtctacttg gtcgatgatg atgatcattt tgatgtgttc ttggatttgg tttgctagga 600
ttttattgag tatttttgca ttgatattca taagggaat tggctcgaag ttctctatcc 660
ttgttggatc c 671

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```

<210> 182
<211> 212
<212> PRT
<213> Mus musculus

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<220>
<221> MOD_RES
<222> (7)
<223> XAA = ANYTHING

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<400> 182
Pro Val Tyr Leu Trp Val Xaa Lys Ala His Leu Val Cys Val Ile Leu
  1             5             10             15

Tyr Gln Ala Thr Ala Leu Lys Leu Phe Ile Trp Phe Arg Ser Ser Leu
          20             25             30

Val Asn Phe Arg Val Thr Tyr Ile Tyr Tyr His Ile Ile Cys Lys Tyr
          35             40             45

Phe Leu Leu Leu Ser Asn Leu Tyr Pro Leu Asp Leu Leu Leu Leu Trp
          50             55             60

Asn Cys Ser Gly Asp Phe Lys Tyr Tyr Ile Glu Val Gly Arg Lys Trp
          65             70             75             80

Gln Leu Val Ser Leu Ile Leu Val Gly Leu Leu Pro Val Ser Ile His
          85             90             95

Leu Leu Cys Trp Leu Leu Val Cys Cys Arg Leu Leu Leu Leu Cys Ser
          100            105            110

Gly Met Gly Leu Glu Phe Leu Ile Phe Pro Arg Leu Leu Ser Met Gly
          115            120            125

Val Gly Phe Cys Gln Met Leu Phe Pro His Leu Met Ile Met Trp Phe
          130            135            140

Leu Ser Leu Ser Leu Leu Leu Trp Ile Thr Met Met Asp Phe Arg Ile
          145            150            155            160

Leu Asn His Pro Cys Ile Pro Gly Met Lys Ser Thr Trp Ser Trp Met
          165            170            175

Ile Ile Leu Met Cys Ser Trp Ile Trp Phe Ala Arg Ile Leu Leu Ser
          180            185            190

```

Ile Phe Ala Leu Ile Phe Ile Arg Glu Ile Gly Leu Lys Phe Ser Ile
 195 200 205

Leu Val Gly Ser
 210

<210> 183
 <211> 637
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (23)..(98)
 <223> N = A, C, G OR T/U

<400> 183
 aagtcaatgt acaaaatgtc tgncaatgcn tcatttaaaa ttaaattggt ttattgagac 60
 agctgtttnt gatgtgtaac gtgaagcaag acagagcctt gttgtgagca gtggcagaag 120
 attttttttt tttaattatt ggtacatatt acccttcaaa tctgagaatt tggactaatt 180
 gcaccaaaga accctctaatt ttggccccctg gcacatgcgt acctgtcaac tttttttctt 240
 ttacaagacc tgcattgctgt cggccatcgc cttctccaat gtttttgagc actatttggg 300
 ggatgacatg aaaagggaaa acccacctgt ggaggacagc agtgatgagg atgacaaaag 360
 aaacccagga aacttgatg acaaggcagg taaagtgagg aagcatgtga cagagcaaga 420
 gaaacctgaa gagggcttgg gcccacaacat caaaagcatt gtgaccatgc tgatgctcat 480
 gctcctgatg atgttcgcgg tccactgcac gtgggtcaca agcaacgcct actccagtcc 540
 aagtgtggtc cttgcctcct acaatcatga tgggtaccagg aatatattag atgattttag 600
 agaagcgtac ttttggtctga gacaaaacac cggatcc 637

<210> 184
 <211> 209
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (8)..(32)
 <223> XAA = ANYTHING

<400> 184
 Ser Gln Cys Thr Lys Cys Leu Xaa Met Xaa His Leu Lys Leu Asn Trp
 1 5 10 15
 Phe Ile Glu Thr Ala Val Xaa Asp Val Arg Glu Ala Arg Gln Ser Xaa
 20 25 30
 Val Val Ser Ser Gly Arg Arg Phe Phe Phe Phe Asn Tyr Trp Tyr Ile
 35 40 45
 Leu Pro Phe Lys Ser Glu Asn Leu Asp Leu His Gln Arg Thr Leu Phe
 50 55 60

Gly Pro Trp His Met Arg Thr Cys Gln Leu Phe Phe Phe Tyr Lys Thr
65 70 75 80

Cys Met Leu Ser Ala Ile Ala Phe Ser Asn Val Phe Glu His Tyr Leu
85 90 95

Gly Asp Asp Met Lys Arg Glu Asn Pro Pro Val Glu Asp Ser Ser Asp
100 105 110

Glu Asp Asp Lys Arg Asn Pro Gly Asn Leu Tyr Asp Lys Ala Gly Lys
115 120 125

Val Arg Lys His Val Thr Glu Gln Glu Lys Pro Glu Glu Gly Leu Gly
130 135 140

Pro Asn Ile Lys Ser Ile Val Thr Met Leu Met Leu Met Leu Leu Met
145 150 155 160

Met Phe Ala Val His Cys Thr Trp Val Thr Ser Asn Ala Tyr Ser Ser
165 170 175

Pro Ser Val Val Leu Ala Ser Tyr Asn His Asp Gly Thr Arg Asn Ile
180 185 190

Leu Asp Asp Phe Arg Glu Ala Tyr Phe Trp Leu Arg Gln Asn Thr Gly
195 200 205

Ser

<210> 185

<211> 669

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (8)..(119)

<223> N = A, C, G OR T/U

<400> 185

cgccccancc aanctgttcg ccaggctaaa ggcgcgcatg ccgacggcga gnatctcgtc 60
gtgacccatg ccgatgcntg cttgccnaat atcatggtga aaatggccgc tttttctgna 120
ttcatcgact gtggccggct ggggtgtggcg gaccgctatc aggacatagc gttggctacc 180
cgtgatattg ctaagagctt ggcggcgaat gggctgaccg cttcctcgtg ctttacggta 240
tcgccgctcc cgattcgcag cgcacgcgct tctatcgctt tcttgacgag ttcttctgaa 300
ttgaaaaaga agagtaagct tgaattcgcg gccgcgtcga ccgcggttac aacctccgga 360
gcgatgcccg tggggggcct gttgccgctc ttcagtagcc ctggggggcg cggcctgggc 420
agtggcctgg gcggggggct tggcggcggg aggaaggggt ctggccccgc tgccttcgcg 480
ctcaccgaga agttcgtgct gctgctggtg ttcagcgctt tcatcacgct ctgcttcggg 540
gcaatcttct tctgcctga ctcctccaag ctgctcagcg gggctcctgtt ccaactccaac 600
cctgccttgc agccgccggc ggagcacaag cccgggctcg gggcgcgctg ggaggatgcc 660
gccggatcc 669

[illegible][illegible]

all other things being equal, men are more likely than women to be violent. This is true even when we control for all the other factors that might influence violence.

(The following are the names of the persons who have been elected to the various offices of the Association.)

[illegible]

all other things being equal, men are more likely than women to be violent.

[illegible]

all other things being equal, men are more likely than women to be involved in violent crime.

[illegible][illegible]

all other things being equal, men are more likely than women to be violent. This is true even if we control for all the other factors that might influence violence.

[illegible]

all other things being equal, men are more likely than women to be violent. But there are many exceptions. In some cultures, women are more violent than men. In some situations, women are more violent than men. In some cases, women are more violent than men.

[illegible][illegible][illegible][illegible]

<210> 187
 <211> 280
 <212> DNA
 <213> Mus musculus

<400> 187
 gaattcgcgg ccgcgtcgac ctcagcttga tctactggac ttgatttgga aaaaaaagtt 60
 ataactttca acaccaactt aaaatgtaat ttccttattt cataaggtgg gggaactgaa 120
 attcatgata tagaaggagc ttaaggtatt atctagggat agttcctccc ttttgggggtt 180
 gattcttata atactttctg taattttctc tataaatatt aatatgtatt tattgtgtgt 240
 gggatatgcat atatatgtat gtatatatga atatggatcc 280

<210> 188
 <211> 217
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (3)..(37)
 <223> XAA = ANYTHING

<400> 188
 His Val Xaa Gly Asn Arg Ser Cys Arg Xaa Gly Xaa Gly Arg Xaa Ser
 1 5 10 15
 Ile Arg Gly Ser Arg Pro Pro Xaa Leu Phe Ala Arg Xaa Lys Ala Arg
 20 25 30
 His Ala Arg Arg Xaa Arg Ser Ser Ser Val Thr His Gly Asp Ala Cys
 35 40 45
 Leu Pro Asn Ile Met Val Lys Met Ala Ala Phe Leu Asn Ser Ser Thr
 50 55 60
 Val Ala Gly Trp Val Trp Arg Pro Leu Ser Asp Ile Ala Leu Ala Thr
 65 70 75 80
 Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu
 85 90 95
 Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr
 100 105 110
 Arg Leu Leu Asp Glu Phe Phe Ile Glu Lys Gly Arg Val Ser Leu Asn
 115 120 125
 Ser Arg Pro Arg Arg Pro Gln Leu Asp Leu Leu Asp Leu Ile Trp Lys
 130 135 140
 Lys Lys Leu Leu Ser Thr Pro Thr Asn Val Ile Ser Leu Phe His Lys
 145 150 155 160
 Val Gly Glu Leu Lys Phe Met Ile Lys Glu Leu Lys Val Leu Ser Arg

165

170

175

Asp Ser Ser Ser Leu Leu Gly Leu Ile Leu Ile Ile Leu Ser Val Ile
 180 185 190

Phe Ser Ile Asn Ile Asn Met Tyr Leu Leu Cys Val Gly Met His Ile
 195 200 205

Tyr Val Cys Ile Tyr Glu Tyr Gly Ser
 210 215

<210> 189

<211> 479

<212> DNA

<213> Mus musculus

<400> 189

gaattcgcgg ccgcgtcgac gagattatga gtttttatgt taataatttc tgattttgta 60
 tagatttttag tcatcattaa ataaaactta cctagttatg tctcagttct caagaaagtc 120
 tgaggaggca aagatgacta tcttctaatt ggttttgagg gattctcatt aatgtgtaac 180
 ctttttgtaa agctgccaaag cctcacagat gagtgtgaag ctagagatgt tgaatcttgc 240
 aggctgcatt accaattctg catcatcatc tagatttttc ctcttatgtc aatgatcatt 300
 tggaaattta ctggtgctgt cttaaaaggg aaatcatgtt taaggattca gataatagaa 360
 tatttaaaaa ttttcaacag atatttcctt tgtgctctct atggacaggt tatttattta 420
 tttactttct gttttgttct gatgtactta ctccatatgc ctggaaagtc cttggatcc 479

<210> 190

<211> 148

<212> PRT

<213> Mus musculus

<400> 190

Ile Arg Gly Arg Val Asp Glu Ile Met Ser Phe Tyr Val Asn Asn Phe
 1 5 10 15

Phe Cys Ile Asp Phe Ser His His Ile Lys Leu Thr Leu Cys Leu Ser
 20 25 30

Ser Gln Glu Ser Leu Arg Arg Gln Arg Leu Ser Ser Asn Trp Phe Gly
 35 40 45

Ile Leu Ile Asn Val Pro Phe Cys Ala Ala Lys Pro His Arg Val Ser
 50 55 60

Arg Cys Ile Leu Gln Ala Ala Leu Pro Ile Leu His His His Leu Asp
 65 70 75 80

Phe Ser Ser Tyr Val Asn Asp His Leu Glu Ile Tyr Trp Cys Cys Leu
 85 90 95

Lys Arg Glu Ile Met Phe Lys Asp Ser Asp Asn Arg Ile Phe Lys Asn
 100 105 110

Phe Gln Gln Ile Phe Pro Leu Cys Ser Leu Trp Thr Gly Tyr Leu Phe
 115 120 125

Ile Tyr Phe Leu Phe Cys Ser Asp Val Leu Thr Pro Tyr Ala Trp Lys
 130 135 140

Val Leu Gly Ser
 145

<210> 191
 <211> 289
 <212> DNA
 <213> Mus musculus

<400> 191
 gaattcgcg cgcgctcgac gccaaagactt cacacagttc tgattgtccc agaagccttg 60
 cgtttgtaaa aacatgacaa tgagatatga aaacttccag aacttggagc gggaagagaa 120
 aaaccaggag atgagaaatg gtgacaagaa aggaggaatg gagtctccaa agtttgctct 180
 aattccttcc cagtccttcc tgtggcgcat cctctcttgg acccacctcc tctgttctc 240
 cctgggcctc agcctcctgc tactggtggt catctccgtg attggatcc 289

<210> 192
 <211> 95
 <212> PRT
 <213> Mus musculus

<400> 192
 Asn Ser Arg Pro Arg Arg Arg Gln Asp Phe Thr Gln Phe Leu Ser Gln
 1 5 10 15

Lys Pro Cys Val Cys Gln Asn Met Thr Met Arg Tyr Glu Asn Phe Gln
 20 25 30

Asn Leu Glu Arg Glu Glu Lys Asn Gln Glu Met Arg Asn Gly Asp Lys
 35 40 45

Lys Gly Gly Met Glu Ser Pro Lys Phe Ala Leu Ile Pro Ser Gln Ser
 50 55 60

Phe Leu Trp Arg Ile Leu Ser Trp Thr His Leu Leu Leu Phe Ser Leu
 65 70 75 80

Gly Leu Ser Leu Leu Leu Val Val Ile Ser Val Ile Gly Ser
 85 90 95

<210> 193
 <211> 658
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base

<222> (24) .. (152)

<223> N = A, C, G OR T/U

<400> 193

```
aaactgacgg catgatgagg acantatgac gaaagtaaag gttacaaaan gagctgagaa 60
cagctgggtc cagtgcgaag anacacggcc aggttggcaa anaggtgcag cggcacaggc 120
cgactcgna gacacatgaa ggatctacgc anccgactcg ggcagtaccg caacgaggtg 180
cacaccatgt tgggccagag cacagaggag atacggggcg ggctctccac acacctgcgc 240
aagatgcgca agcgcttgat gcgggatgcc gaggatctgc agaagcgcct agcttggtga 300
caaggcaggg gcacgcgagg gcgcgcgagg cgggtgtgagt gccatccgtg agcgccctggg 360
gcctctgggt gagcaagggt gccagcgcac cgccaaccta ggcgctgggg ccgcccagcc 420
tctgcgcgat cgcgcccagg cttttgggtga ccgcatccga gggcggctgg aggaagtggg 480
caaccaggcc cgtgaccgcc tagaggaggt gcgtgagcac atggaggagg tgcgctccaa 540
gatggaggaa ctctcgagtc ccagcatcag agcgcgtgga ctttttcccg cgtcccgcag 600
catgcaggtc tcccgtgtgc tggccgcgct gtgcggcatg ctactctgcg ccggatcc 658
```

<210> 194

<211> 215

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (7) .. (49)

<223> XAA = ANYTHING

<400> 194

```
Asn Arg His Asp Glu Asp Xaa Met Thr Lys Val Lys Val Thr Lys Xaa
  1                      5                      10                      15
```

```
Ala Glu Asn Ser Trp Val Gln Cys Glu Xaa Thr Arg Pro Gly Trp Gln
                20                      25                      30
```

```
Xaa Gly Ala Ala Ala Gln Ala Asp Ser Xaa Pro Thr Arg Ile Tyr Ala
        35                      40                      45
```

```
Xaa Asp Ser Gly Ser Thr Ala Thr Arg Cys Thr Pro Cys Trp Ala Arg
        50                      55                      60
```

```
Ala Gln Arg Arg Tyr Gly Arg Gly Ser Pro His Thr Cys Ala Arg Cys
        65                      70                      75                      80
```

```
Ala Ser Ala Cys Gly Met Pro Arg Ile Cys Arg Ser Ala Leu Val Tyr
                85                      90                      95
```

```
Lys Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Val Ser Ala Ile Arg
        100                      105                      110
```

```
Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Gln Arg Thr Ala Asn
        115                      120                      125
```

```
Leu Gly Ala Gly Ala Ala Gln Pro Leu Arg Asp Arg Ala Gln Ala Phe
        130                      135                      140
```

Gly Asp Arg Ile Arg Gly Arg Leu Glu Glu Val Gly Asn Gln Ala Arg
145 150 155 160

Asp Arg Leu Glu Glu Val Arg Glu His Met Glu Glu Val Arg Ser Lys
165 170 175

Met Glu Glu Leu Ser Ser Pro Ser Ile Arg Ala Arg Gly Pro Phe Pro
180 185 190

Ala Ser Arg Ser Met Gln Val Ser Arg Val Leu Ala Ala Leu Cys Gly
195 200 205

Met Leu Leu Cys Ala Gly Ser
210 215

<210> 195

<211> 412

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (14)

<223> N = A, C, G OR T/U

<400> 195

```
gaattcgcgg cggngggcgac cttttttttt tttttttttt tttttttttt tttttttttt 60
tttccaagat aaaactttat tggagacagc aaggagtata ctgaaagtgg gggagccatg 120
ccttcattcc ataactgcaa tcagatgctc tcctctgaga gagagtgtgt ggggagccaa 180
ggtgagaagc aggtatgatt cacaccccaa ctgcttggag agtgcttata tgacagtctt 240
tttctcgatt ttattttttt tcagttcttc aacacacact ttggcttcat ttgggggaaa 300
attaacaaa agaacagaat ttccctcccc cagagttact tatgaaatga cacagctgcc 360
cttttctttg aagggtattct tgtcttctgg gattcccttt accagaggat cc 412
```

<210> 196

<211> 670

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (43) .. (107)

<223> N = A, C, G, OR T/U

<400> 196

```
acaagcccta gccttgtgtc atggcttcaa tttggacatt gancatccca tgacnttcca 60
agagaatgca aaagnctttg nacagagtgt ggtccagctt ggcggancca gtgtggttgt 120
tgcagccccc cagaaggcaa aggtgtgtaa ccagacaggt gccctctacc agtgtgacta 180
cagcacaagc cgggtgtgacc ccatccccct gcaagtacct ccagaggctg tgaatatgtc 240
cttggggcctg tccttggctg tttctactgt cccccagcag ctgctggcct gtggccccac 300
ggtgcaccaa aactgcaagg agaatactta tgtgaatgga ttgtgctatt tgttcggctc 360
caacctgctg aggccgcccc agcagttccc agaggctctc agagaatgtc ctcagcagga 420
gagtgcatt gtcttcttga ttgatggctc cggtagcatc aacaacattg actttcagaa 480
```

gatgaaggag tttgtctcaa ctgtgatgga gcagttcaaa aagtctaaaa ccttgttctc 540
 tttgatgcag tactcggacg agttccggat tcacttcacc ttcaatgact tcaagagaaa 600
 ccctagccca agatcacacg tgagcccat aaagcagctg aatgggagga caaaaactgc 660
 ctcggatcc 670

<210> 197
 <211> 223
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (14) .. (36)
 <223> XAA = ANYTHING

<400> 197

Gln	Ala	Leu	Ala	Leu	Cys	His	Gly	Phe	Asn	Leu	Asp	Ile	Xaa	His	Pro	1	5	10	15
Met	Thr	Phe	Gln	Glu	Asn	Ala	Lys	Xaa	Phe	Xaa	Gln	Ser	Val	Val	Gln	20	25	30	
Leu	Gly	Gly	Xaa	Ser	Val	Val	Val	Ala	Ala	Pro	Gln	Lys	Ala	Lys	Ala	35	40	45	
Val	Asn	Gln	Thr	Gly	Ala	Leu	Tyr	Gln	Cys	Asp	Tyr	Ser	Thr	Ser	Arg	50	55	60	
Cys	Asp	Pro	Ile	Pro	Leu	Gln	Val	Pro	Pro	Glu	Ala	Val	Asn	Met	Ser	65	70	75	80
Leu	Gly	Leu	Ser	Leu	Ala	Val	Ser	Thr	Val	Pro	Gln	Gln	Leu	Leu	Ala	85	90	95	
Cys	Gly	Pro	Thr	Val	His	Gln	Asn	Cys	Lys	Glu	Asn	Thr	Tyr	Val	Asn	100	105	110	
Gly	Leu	Cys	Tyr	Leu	Phe	Gly	Ser	Asn	Leu	Leu	Arg	Pro	Pro	Gln	Gln	115	120	125	
Phe	Pro	Glu	Ala	Leu	Arg	Glu	Cys	Pro	Gln	Gln	Glu	Ser	Asp	Ile	Val	130	135	140	
Phe	Leu	Ile	Asp	Gly	Ser	Gly	Ser	Ile	Asn	Asn	Ile	Asp	Phe	Gln	Lys	145	150	155	160
Met	Lys	Glu	Phe	Val	Ser	Thr	Val	Met	Glu	Gln	Phe	Lys	Lys	Ser	Lys	165	170	175	
Thr	Leu	Phe	Ser	Leu	Met	Gln	Tyr	Ser	Asp	Glu	Phe	Arg	Ile	His	Phe	180	185	190	
Thr	Phe	Asn	Asp	Phe	Lys	Arg	Asn	Pro	Ser	Pro	Arg	Ser	His	Val	Ser	195	200	205	

Pro Ile Lys Gln Leu Asn Gly Arg Thr Lys Thr Ala Ser Gly Ser
 210 215 220

<210> 198
 <211> 640
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (21)
 <223> N = A, C, G OR T/U

<400> 198
 ctgttgatgg cttttacatg nacgcctatg aagtcagcaa tgcggatttt gagaagtttg 60
 tgaactcgac tggctatttg acagagctga gaagtttgaa gactctttcg tctttgaagg 120
 catggttgagc gagcaagtga aaacgcatat ccaccaggca gttgcagctg ctccatggtg 180
 gttgcctgtc aaggagagcta attggagaca cccagagggg cgggactcca gtattctgca 240
 caggtcaaatt catccgggttc tccatgtttc ctggaacgat gctggtgcct actgcacatg 300
 ggcgggcaag aggttgacct ctgaggcaga gtgggaatac agctgtagag gaggcctgca 360
 gaacaggctt tccccctggg gcaacaaact gcagcccaaa ggacagcatt atgccaacat 420
 ctggcagggc aagtttccctg tgagcaacac tggcgaggat ggcttccaag gaactgcccc 480
 cggttgatgcc tttcctccca atggctatgg cttatacaac atagtgggga atgtgtggga 540
 gtggacctca gactggtgga ctgttcacca ttctgttgag gaaacgttca acccaaaggg 600
 tcccacttct gggaaagacc gagtgaagaa ggggtgatcc 640

<210> 199
 <211> 210
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (6)
 <223> XAA = ANYTHING

<400> 199
 Cys Trp Leu Leu His Xaa Arg Leu Ser Gln Gln Cys Gly Phe Glu Val
 1 5 10 15
 Cys Glu Leu Asp Trp Leu Phe Asp Arg Ala Glu Lys Phe Glu Asp Ser
 20 25 30
 Phe Val Phe Glu Gly Met Leu Ser Glu Gln Val Lys Thr His Ile His
 35 40 45
 Gln Ala Val Ala Ala Ala Pro Trp Trp Leu Pro Val Lys Gly Ala Asn
 50 55 60
 Trp Arg His Pro Glu Gly Pro Asp Ser Ser Ile Leu His Arg Ser Asn
 65 70 75 80

His Pro Val Leu His Val Ser Trp Asn Asp Ala Val Ala Tyr Cys Thr
85 90 95

Trp Ala Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser Cys
100 105 110

Arg Gly Gly Leu Gln Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu Gln
115 120 125

Pro Lys Gly Gln His Tyr Ala Asn Ile Trp Gln Gly Lys Phe Pro Val
130 135 140

Ser Asn Thr Gly Glu Asp Gly Phe Gln Gly Thr Ala Pro Val Asp Ala
145 150 155 160

Phe Pro Pro Asn Gly Tyr Gly Leu Tyr Asn Ile Val Gly Asn Val Trp
165 170 175

Glu Trp Thr Ser Asp Trp Trp Thr Val His His Ser Val Glu Glu Thr
180 185 190

Phe Asn Pro Lys Gly Pro Thr Ser Gly Lys Asp Arg Val Lys Lys Gly
195 200 205

Gly Ser
210

<210> 200

<211> 263

<212> DNA

<213> Mus musculus

<400> 200

gaattcgcg cgcgcgcgac ggccagcctg gtctacagag tggattcctg tcctgtcagg 60
gctgcacgat gagtccctat ctcaaagaag aagaaaaaaa aaaaagaaag aaagaaagac 120
ttctttttga aatattagac aaccaatatg acaaaatagc aatgccaaac atcctgctgt 180
accgtacgat ctatttttgt tttttttttt ggttggtgtt cttgaccaa ataaatgatt 240
accggaggca atcacatgga tcc 263

<210> 201

<211> 87

<212> PRT

<213> Mus musculus

<400> 201

Ile Arg Gly Arg Val Asp Gly Gln Pro Gly Leu Gln Ser Gly Phe Leu
1 5 10 15

Ser Cys Gln Gly Cys Thr Met Ser Pro Tyr Leu Lys Glu Glu Glu Lys
20 25 30

Lys Lys Arg Lys Lys Glu Arg Leu Leu Phe Glu Ile Leu Asp Asn Gln
35 40 45

Tyr Asp Lys Ile Arg Met Pro Asn Ile Leu Leu Tyr Arg Thr Ile Tyr
 50 55 60

Phe Cys Phe Phe Phe Trp Leu Leu Phe Leu Thr Lys Ile Asn Asp Tyr
 65 70 75 80

Arg Arg Gln Ser His Gly Ser
 85

<210> 202
 <211> 544
 <212> DNA
 <213> Mus musculus

<400> 202
 gaattcgcg cgcgctcgac ctgtacgatt gtcagtggat ctgacgacac caaaagggct 60
 caggatgcta ctggtgcaag ctctcctgtt cctcttaatc ctgcccagtc atgccgaaga 120
 tgacgttact acaactgaag agctagctcc tgctttggtc cctccacca agggaacttg 180
 tgcaggttgg atggcaggca tcccaggaca tcctggccac aatggcacac caggccgtga 240
 tggcagagat ggcactcctg gagagaaggg agagaaagga gatgcaggtc ttcttgggtcc 300
 taagggtgag acaggagatg ttggaatgac aggagctgaa gggccacggg gcttccccgg 360
 aaccctggc aggaaaggag agcctggaga agccgcttat gtgtatcgct cagcgttcag 420
 tgtggggctg gagaccgcg tcaactgttc caatgtaccc attcgcttta ctaagatctt 480
 ctacaaccaa cagaatcatt atgacggcag cactggcaag ttctactgca acattccagg 540
 atcc 544

<210> 203
 <211> 181
 <212> PRT
 <213> Mus musculus

<400> 203
 Asn Ser Arg Pro Arg Arg Pro Val Arg Leu Ser Val Asp Leu Thr Thr
 1 5 10 15
 Pro Lys Gly Leu Arg Met Leu Leu Leu Gln Ala Leu Leu Phe Leu Leu
 20 25 30
 Ile Leu Pro Ser His Ala Glu Asp Asp Val Thr Thr Thr Glu Glu Leu
 35 40 45
 Ala Pro Ala Leu Val Pro Pro Pro Lys Gly Thr Cys Ala Gly Trp Met
 50 55 60
 Ala Gly Ile Pro Gly His Pro Gly His Asn Gly Thr Pro Gly Arg Asp
 65 70 75 80
 Gly Arg Asp Gly Thr Pro Gly Glu Lys Gly Glu Lys Gly Asp Ala Gly
 85 90 95
 Leu Leu Gly Pro Lys Gly Glu Thr Gly Asp Val Gly Met Thr Gly Ala
 100 105 110

Glu Gly Pro Arg Gly Phe Pro Gly Thr Pro Gly Arg Lys Gly Glu Pro
115 120 125

Gly Glu Ala Ala Tyr Val Tyr Arg Ser Ala Phe Ser Val Gly Leu Glu
130 135 140

Thr Arg Val Thr Val Pro Asn Val Pro Ile Arg Phe Thr Lys Ile Phe
145 150 155 160

Tyr Asn Gln Gln Asn His Tyr Asp Gly Ser Thr Gly Lys Phe Tyr Cys
165 170 175

Asn Ile Pro Gly Ser
180

<210> 204

<211> 244

<212> DNA

<213> Mus musculus

<400> 204

gaattcgcgg ccgcgtcgac cattatTTTT ggttggttgt cttggggttag cattaaagcc 60
ttcacctatt tatggagggt taggtttaat tgtagtggtg tttggttggt gtttaatggt 120
tttaggggtt ggtggatcgt ttttaggttt aatagtttt ttaatttatt taggggggat 180
gttggttgtg tttggatata cgactgctat agctactgag gaatatccag agacttgttg 240
atcc 244

<210> 205

<211> 81

<212> PRT

<213> Mus musculus

<400> 205

Asn Ser Arg Pro Arg Arg Pro Leu Phe Leu Val Gly Cys Leu Gly Leu
1 5 10 15

Ala Leu Lys Pro Ser Pro Ile Tyr Gly Gly Leu Gly Leu Ile Val Ser
20 25 30

Gly Phe Val Gly Cys Leu Met Val Leu Gly Phe Gly Gly Ser Phe Leu
35 40 45

Gly Leu Ile Val Phe Leu Ile Tyr Leu Gly Gly Met Leu Val Val Phe
50 55 60

Gly Tyr Thr Thr Ala Ile Ala Thr Glu Glu Tyr Pro Glu Thr Cys Gly
65 70 75 80

Ser

<210> 206
 <211> 244
 <212> DNA
 <213> Mus musculus

<400> 206
 gaattcgcgg ccgcgtcgac cattatTTTT ggttggttgt cttggggttag cattaaagcc 60
 ttcacctatt tatggagggt taggtttaat tgtagtgagg tttggttggt gttaaatggt 120
 tttagggttt ggtggatcgt ttttaggttt aatagttttt ttaatttatt taggggggat 180
 gttggttggt tttggatata cgactgctat agctactgag gaatatccag agacttgtgg 240
 atcc 244

<210> 207
 <211> 81
 <212> PRT
 <213> Mus musculus

<400> 207
 Asn Ser Arg Pro Arg Arg Pro Leu Phe Leu Val Gly Cys Leu Gly Leu
 1 5 10 15
 Ala Leu Lys Pro Ser Pro Ile Tyr Gly Gly Leu Gly Leu Ile Val Ser
 20 25 30
 Gly Phe Val Gly Cys Leu Met Val Leu Gly Phe Gly Gly Ser Phe Leu
 35 40 45
 Gly Leu Ile Val Phe Leu Ile Tyr Leu Gly Gly Met Leu Val Val Phe
 50 55 60
 Gly Tyr Thr Thr Ala Ile Ala Thr Glu Glu Tyr Pro Glu Thr Cys Gly
 65 70 75 80
 Ser

<210> 208
 <211> 235
 <212> DNA
 <213> Mus musculus

<400> 208
 gaattcgcgg ccgcgtcgac ctagtgtgct ctttgagatt tttaagagca ttgagatac 60
 aagaattttg aggggatgag gaatgttggt caaggtctaa atcacacata aaaaattttc 120
 ttctgtgaat ttatcttctt tgcataatata tccctgctgg ccccttggtt tgattttggt 180
 attggtcatt ccagctotca gtggaagacc ggaccctgtc attcatgaag gatcc 235

<210> 209
 <211> 675
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (81)..(267)
 <223> N = A, C, G OR T/U

<400> 209

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gaattcgcgg ccgcgtcgac ccacgttttt tgaccacaaa ccgcaagttt tagatcctcg 60
cgagtaggaa atgaaggggt nccacacaga aggcagcgcc cactgggctc cactgatgca 120
ggttgcccac cagaccacat cactctggcc ctgggctcag ggcatgatgt gagtgtgaga 180
gctttggccc ggttgccatt aagactcact ccaggtcaca ctgagggcaa gggttgctag 240
tccctggccg ctgggactct ctcatcntga gttctcccat caccatcact aagaatgttt 300
ttctggtaac cgaagttgaa ttgagacatc caaggtcatc tatgcatttg gacaagattc 360
agacatctag gcggtctgtc cggctttacc ggggagaatc taaaaaagaa gcacattcat 420
cctccattat tttgatgtca tatctaagac aaaatgtcaa taaatgaagt atcaacattc 480
tatatcataa aagaagatac aattgcaatg ggaggtgcac aaataatgct tggcctaatt 540
cacaatgcac tggggactct ctggctctct ttgcacaatc tagaagacaa gagatatagc 600
atcggccata aacttatgtt agctagtatc tgctacctgt ttgtgtctgg aacatttttc 660
atcaactcag gatcc                                     675
  
```

<210> 210
 <211> 218
 <212> PRT
 <213> Mus musculus

<400> 210

```

Glu Phe Ala Ala Ala Ser Thr His Val Phe Pro Thr Thr Ala Ser Phe
  1                      5                      10                      15

Arg Ser Ser Arg Val Gly Asn Glu Gly Val Pro His Arg Arg Gln Arg
          20                      25                      30

Pro Leu Gly Ser Thr Asp Ala Gly Cys Pro Pro Asp His Ile Thr Leu
          35                      40                      45

Ala Leu Gly Ser Gly His Asp Val Ser Val Arg Ala Leu Ala Arg Leu
          50                      55                      60

Pro Leu Arg Leu Thr Pro Gly His Thr Glu Gly Lys Gly Cys Ser Leu
          65                      70                      75                      80

Ala Ala Gly Thr Leu Ser Ser Val Leu Pro Ser Pro Ser Leu Arg Met
          85                      90                      95

Phe Phe Trp Pro Lys Leu Asn Asp Ile Gln Gly His Leu Cys Ile Trp
          100                     105                     110

Thr Arg Phe Arg His Leu Gly Gly Leu Ser Gly Phe Thr Gly Glu Asn
          115                     120                     125

Leu Lys Lys Lys His Ile His Pro Pro Leu Phe Cys His Ile Asp Lys
          130                     135                     140

Met Ser Ile Asn Glu Val Ser Thr Phe Tyr Ile Ile Lys Glu Asp Thr
          145                     150                     155                     160
  
```

Ile Ala Met Gly Gly Ala Gln Ile Met Leu Gly Leu Ile His Asn Ala
165 170 175

Leu Gly Thr Leu Trp Leu Ser Leu His Asn Leu Glu Asp Lys Arg Tyr
180 185 190

Ser Ile Gly His Lys Leu Met Leu Ala Ser Ile Cys Tyr Leu Phe Val
195 200 205

Ser Gly Thr Phe Phe Ile Asn Ser Gly Ser
210 215

<210> 211

<211> 630

<212> DNA

<213> Mus musculus

<400> 211

gaattcgcgg cccgcgtcga cgtcactgtg gagctcagat cacagtgcgtg acagaatcca 60
tatttggaga attacataag gtttgaaaga gaggatagtg aaaggatacg aattcctaaa 120
aacgtttaat ctggcctttt gtttgaacga aagagaaatt gaaaccaaatt gaaataaatt 180
acttgttaga aagaatactg ccaacagcat agcaaaaatga aattcttcct gctgctttcc 240
ctcattggat tctgctgggc ccaatatgac ccacatactc aatatggacg aactgctatt 300
gtccacctgt ttgagtggcg ctgggttgat attgctaagg aatgtgagag atacttagct 360
cctaattgat ttgcaggtgt gcaggtctct ccaccaatg aaaacatcgt agtccacagc 420
ccttcaagac catggtggga aagatatcaa ccaattagct acaaaatatg ttccaggtct 480
ggaaatgaag atgaattcag ggacatgggtg aacaggtgca acaatgttgg tgtccgtatt 540
tatgtggatg ctgtcattaa ccacatgtgt ggagtggggg ctcaagctgg acaaagcagt 600
acatgtggaa gttatttcaa ccccgatcc 630

<210> 212

<211> 205

<212> PRT

<213> Mus musculus

<400> 212

Glu Phe Ala Ala Arg Val Asp Val Thr Val Glu Leu Arg Ser Gln Cys
1 5 10 15

Gln Asn Pro Tyr Leu Glu Asn Tyr Ile Arg Phe Glu Arg Glu Asp Ser
20 25 30

Glu Arg Ile Arg Ile Pro Lys Asn Val Ser Gly Leu Leu Phe Glu Arg
35 40 45

Lys Arg Asn Asn Gln Met Lys Ile Thr Cys Lys Glu Tyr Cys Gln Gln
50 55 60

His Ser Lys Met Lys Phe Phe Leu Leu Leu Ser Leu Ile Gly Phe Cys
65 70 75 80

Trp Ala Gln Tyr Asp Pro His Thr Gln Tyr Gly Arg Thr Ala Ile Val

85

90

95

His Leu Phe Glu Trp Arg Trp Val Asp Ile Ala Lys Glu Cys Glu Arg
 100 105 110

Tyr Leu Ala Pro Asn Gly Phe Ala Gly Val Gln Val Ser Pro Pro Asn
 115 120 125

Glu Asn Ile Val Val His Ser Pro Ser Arg Pro Trp Trp Glu Arg Tyr
 130 135 140

Gln Pro Ile Ser Tyr Lys Ile Cys Ser Arg Ser Gly Asn Glu Asp Glu
 145 150 155 160

Phe Arg Asp Met Val Asn Arg Cys Asn Asn Val Gly Val Arg Ile Tyr
 165 170 175

Val Asp Ala Val Ile Asn His Met Cys Gly Val Gly Ala Gln Ala Gly
 180 185 190

Gln Ser Ser Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser
 195 200 205

<210> 213

<211> 370

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (337)

<223> N = A, C, G, OR T/U

<400> 213

gaattcgcgg ccgcgtcgac gtaaaaggcc taggagattt gttgatccaa taaatatgat 60
 tagggaaaca attattaggg ttcattgttcg tccttttggt gtgtggatta gcattatttg 120
 tttgataata agtttaacta gctggttgga ggttttgccg tcggccgaga agacggcact 180
 gctgcaggat gggaagagga tgggtgacta tttgttccca gacgggaagg aaatggcaga 240
 agaatatgac gagaagacca gtgaactcct tgtgaggaag tggcgtgtga aaaatgccct 300
 gggagccttg ggccagtggc agcttgaagt gggagancca gtgccctcag gagctgggag 360
 cctgggatcc 370

<210> 214

<211> 123

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (112)

<223> XAA = ANYTHING

<400> 214

Asn Ser Arg Pro Arg Arg Arg Lys Arg Pro Arg Arg Phe Val Asp Pro
 1 5 10 15
 Ile Asn Met Ile Arg Glu Thr Ile Ile Arg Val His Val Arg Pro Phe
 20 25 30
 Gly Val Trp Ile Ser Ile Ile Cys Leu Ile Ile Ser Leu Thr Ser Trp
 35 40 45
 Leu Glu Val Leu Arg Ser Ala Glu Lys Thr Ala Leu Leu Gln Asp Gly
 50 55 60
 Lys Arg Met Val His Tyr Leu Phe Pro Asp Gly Lys Glu Met Ala Glu
 65 70 75 80
 Glu Tyr Asp Glu Lys Thr Ser Glu Leu Leu Val Arg Lys Trp Arg Val
 85 90 95
 Lys Asn Ala Leu Gly Ala Leu Gly Gln Trp Gln Leu Glu Val Gly Xaa
 100 105 110
 Pro Val Pro Ser Gly Ala Gly Ser Leu Gly Ser
 115 120

<210> 215

<211> 508

<212> DNA

<213> Mus musculus

<400> 215

gaattcgcgg ccgcgtcgac gagatcgaga aattcgataa gtcgaagttg aagaaaacag 60
 aaacgcaaga gaaaaatcct ctgccttcaa aagaaacaat tgaacaagag aagcaagctg 120
 gcgaatcgta atgaggcgag cgccgccaat atgcactgta cattccacga gcattgcctt 180
 cttatttttac ttcttttagc tgtttaactt tgtaagatgc aaagagggtg gatcaagttt 240
 aaatgactgt gctgccccctt tcacatcaaa gaatcagaac tactgagcag gaaggcctcc 300
 cctgcctctc ccacccatct gatggtcttg ctagcagaga gggaaaagaa cttgcatggt 360
 ggtgaaggaa aaagctgggt gggagatgat gaaatagaga ggaaaattca agatggtcaa 420
 agatgtcctg caggatgtaa aatgcagttt aatcagagtgc ccattttttt ttgttcaaac 480
 aattttaatt attggaatgc acggatcc 508

<210> 216

<211> 162

<212> PRT

<213> Mus musculus

<400> 216

Asn Ser Arg Pro Arg Arg Arg Asp Arg Glu Ile Arg Val Glu Val Glu
 1 5 10 15
 Glu Asn Arg Asn Ala Arg Glu Lys Ser Ser Ala Phe Lys Arg Asn Asn
 20 25 30
 Thr Arg Glu Ala Ser Trp Arg Ile Val Met Arg Arg Ala Pro Pro Ile

35

40

45

Cys Thr Val His Ser Thr Ser Ile Ala Phe Leu Phe Tyr Phe Phe Leu
50 55 60

Phe Asn Phe Val Arg Cys Lys Glu Val Gly Ser Ser Leu Asn Asp Cys
65 70 75 80

Ala Ala Pro Phe Thr Ser Lys Asn Gln Asn Tyr Ala Gly Arg Pro Pro
85 90 95

Leu Pro Leu Pro Pro Ile Trp Ser Gly Gln Arg Gly Lys Arg Thr Cys
100 105 110

Met Leu Val Lys Glu Lys Ala Gly Trp Glu Met Met Lys Arg Gly Lys
115 120 125

Phe Lys Met Val Lys Asp Val Leu Gln Asp Val Lys Cys Ser Leu Ile
130 135 140

Arg Val Pro Phe Phe Phe Val Gln Thr Ile Leu Ile Ile Gly Met His
145 150 155 160

Gly Ser

<210> 217

<211> 920

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (2)..(302)

<223> N = A, C, G OR T/U

<400> 217

tntngaattc cccagttaan agaatttggc ccaataggnc cccgggaccg gtntngngng 60
antcgatgtt gccaaaccag gntcncaang ttttgtaacc cngaagatga ggaggactac 120
tnnttttcgg aagccttaag gcatnaacgt cagacagnaa naaagtgtcc aagtgggact 180
gccgntcttc taccaatccc agccgaagaa tgctcctgtg accttcattg tgnatgganc 240
agtagtgaaa ttgcccgaag gcttgggaaa nccaatatat atactcagaa ccaagagcct 300
cntaagaagg tatgatgacc aaaaggacta aagacatggg caagttcagc tctgttactg 360
tgtctaccca ttgatgaaga agaagaggag atagaggcta ggggaagttgc tgactcttac 420
gcgcagaatg ccaaagtgat tgaaaagcag ctggagcgca aaggcatgag caagaggagg 480
ctgcaggagt tggttgaatt ggaagccaag aaagcaaaaa tgaaggggac cctgatcgac 540
aatcagttca aataatcaag atctttcttg gttcagactg gaggcagcag ttagatgagg 600
aagagtagct tcaagatgtg ttttcgtttc tgtttctccc agaagggttt tctgaccatc 660
ctattggttt tctgacactt tttcttttct tccattgaag tccttgactc catttcaact 720
gctttctagg aggtagattg tttgtaaaat ctctgtatat atgttttctg tctttcttgt 780
ctttgagatc aggtcttgtt acataccaga gtatggcctt gaactttgtg agcctcctct 840
cctgtcttag tctctctctc tctctctctc tctctctctc tctctctctg ctgaagttcc 900
aggaccacac caccgatcc 920

<210> 218
 <211> 291
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (1)..(85)
 <223> XAA = ANYTHING

<400> 218

Xaa Asn Ser Pro Val Xaa Arg Ile Trp Pro Asn Arg Xaa Pro Gly Pro
 1 5 10 15

Val Xaa Xaa Xaa Ser Met Leu Pro Asn Gln Xaa Xaa Xaa Val Leu Pro
 20 25 30

Xaa Arg Gly Gly Leu Leu Xaa Phe Gly Ser Leu Lys Ala Xaa Thr Ser
 35 40 45

Asp Xaa Xaa Lys Val Ser Lys Trp Asp Cys Arg Ser Ser Thr Asn Pro
 50 55 60

Ser Arg Arg Met Leu Leu Pro Ser Leu Xaa Met Xaa Gln Asn Leu Pro
 65 70 75 80

Lys Ala Trp Glu Xaa Gln Tyr Ile Tyr Ser Glu Pro Arg Ala Ser Glu
 85 90 95

Gly Met Met Thr Lys Arg Thr Lys Asp Met Gly Lys Phe Ser Ser Val
 100 105 110

Thr Val Ser Thr His Arg Arg Arg Gly Asp Arg Gly Gly Ser Cys Leu
 115 120 125

Leu Arg Ala Glu Cys Gln Ser Asp Lys Ala Ala Gly Ala Gln Arg His
 130 135 140

Glu Gln Glu Glu Ala Ala Gly Val Gly Ile Gly Ser Gln Glu Ser Lys
 145 150 155 160

Asn Glu Gly Asp Pro Asp Arg Gln Ser Val Gln Ile Ile Lys Ile Phe
 165 170 175

Leu Gly Ser Asp Trp Arg Gln Gln Leu Asp Glu Glu Glu Leu Gln Asp
 180 185 190

Val Phe Ser Phe Leu Phe Leu Pro Glu Gly Phe Ser Asp His Pro Ile
 195 200 205

Gly Phe Leu Thr Leu Phe Leu Phe Phe His Ser Pro Leu His Phe Thr
 210 215 220

Cys Phe Leu Gly Gly Arg Leu Phe Val Lys Ser Leu Tyr Ile Cys Phe

Glu Ser Val Trp Gly Ala Lys Val Arg Ser Arg Tyr Asp Ser His Pro
50 55 60

Asn Cys Leu Glu Ser Ala Tyr Met Thr Val Phe Phe Ser Ile Leu Phe
65 70 75 80

Phe Leu Ser Ser Ser Thr His Thr Leu Ala Ser Phe Gly Gly Lys Leu
85 90 95

Asn Lys Arg Thr Glu Phe Pro Ser Pro Arg Val Thr Tyr Glu Met Thr
100 105 110

Gln Leu Pro Phe Ser Leu Lys Gly Phe Leu Ser Ser Gly Ile Pro Phe
115 120 125

Thr Arg Gly Ser
130

<210> 221
<211> 244
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (210)
<223> N = A, C, G OR T/U

<400> 221
gaattcgcgg ccgcgtcgac ggagtccttct gactgctggt ggagcaggtc tcaggaatct 60
cttcgcttca gcttcaatca tggcctgtgg tctggtcgcc agcaacctga atctcaaacc 120
tggggaatgt ctcaaagttc ggggagaggt ggcctcggac gccaaagagct ttgtgctgaa 180
cctgggaaaa gacagcaaca acctgtgccn acacttcaat cctcgcttca atgcacatgg 240
atcc 244

<210> 222
<211> 81
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (70)
<223> XAA = ANYTHING

<400> 222
Asn Ser Arg Pro Arg Arg Arg Ser Leu Leu Thr Ala Gly Gly Ala Gly
1 5 10 15

Leu Arg Asn Leu Phe Ala Ser Ala Ser Ile Met Ala Cys Gly Leu Val
20 25 30

Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Lys Val Arg Gly

35

40

45

Glu Val Ala Ser Asp Ala Lys Ser Phe Val Leu Asn Leu Gly Lys Asp
50 55 60

Ser Asn Asn Leu Cys Xaa His Phe Asn Pro Arg Phe Asn Ala His Gly
65 70 75 80

Ser

<210> 223

<211> 142

<212> DNA

<213> Mus musculus

<400> 223

gaattcgcgg ccgcgtcgac gttcattatt tttggttggt tgtcttgggt tagcattaaa 60
gccttcacct atttatggag gtttaggttt aattgtagt gggtttggtt gttgtttaat 120
ggtttttagg tttggtggat cc 142

<210> 224

<211> 55

<212> PRT

<213> Mus musculus

<400> 224

Ile Glu Lys Gly Arg Val Ser Leu Asn Ser Arg Pro Arg Arg Arg Ser
1 5 10 15

Leu Phe Leu Val Gly Cys Leu Gly Leu Ala Leu Lys Pro Ser Pro Ile
20 25 30

Tyr Gly Gly Leu Gly Leu Ile Val Ser Gly Phe Val Gly Cys Leu Met
35 40 45

Val Leu Gly Phe Gly Gly Ser
50 55

<210> 225

<211> 394

<212> DNA

<213> Mus musculus

<400> 225

gaattcgcgg ccgcgtcgac tttttttttt ttttttttga tttttccaag ataaaacttt 60
attggagaca gcaaggagta tactgaaagt gggggagcca tgccttcatt ccataactgc 120
aatcagatgc tctcctctga gagagagtgt gtggggagcc aagggtgagaa gcaggtatga 180
ttcacacccc aactgcttgg agagtgttta tatgacagtc tttttctcga ttttattttt 240
tctcagttct tcaacacaca ctttggcttc atttggggga aaattaaaca aaagaacaga 300
atttccctcc cccagagtta cttatgaaat gacacagctg cccttttctt tgaagggatt 360
cttgtcttct gggattccct ttaccagagg atcc 394

<210> 226
 <211> 130
 <212> PRT
 <213> Mus musculus

<400> 226
 Asn Ser Arg Pro Arg Arg Leu Phe Phe Phe Phe Phe Phe Gln Asp
 1 5 10 15
 Lys Thr Leu Leu Glu Thr Ala Arg Ser Ile Leu Lys Val Gly Glu Pro
 20 25 30
 Cys Leu His Ser Ile Thr Ala Ile Arg Cys Ser Pro Leu Arg Glu Ser
 35 40 45
 Val Trp Gly Ala Lys Val Arg Ser Arg Tyr Asp Ser His Pro Asn Cys
 50 55 60
 Leu Glu Ser Ala Tyr Met Thr Val Phe Phe Ser Ile Leu Phe Phe Leu
 65 70 75 80
 Ser Ser Ser Thr His Thr Leu Ala Ser Phe Gly Gly Lys Leu Asn Lys
 85 90 95
 Arg Thr Glu Phe Pro Ser Pro Arg Val Thr Tyr Glu Met Thr Gln Leu
 100 105 110
 Pro Phe Ser Leu Lys Gly Phe Leu Ser Ser Gly Ile Pro Phe Thr Arg
 115 120 125
 Gly Ser
 130

<210> 227
 <211> 480
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (21)..(36)
 <223> N - A, C, G OR T/U

<400> 227
 gaattcgcg cgcgctcgac nttttttttt tttttntttt tttttttttt tttttttttt 60
 ttttaagaaca actgaacata tggtgtgtgt accgggcata aaggatgaat gggcccttta 120
 gttaaccac tgcttgata acatgacact tagtccactt ccatctctcc ggagtcggtg 180
 tgctgtgagc ttcctttggg tggatctggg ctggtctctg aaccactctg tccgtccatt 240
 ggtccattgt gtcactacc agtttttgc tttgtctcag gagcttctac ttttggtttg 300
 ggcttataaa cgatggggtt acagaaatta tccagttcct ttgactttgt aactatttct 360
 gacactttta ccacgggata ttgagtgaga cttaatttat tctgtgcatt catcttactg 420
 tttageccagt tcatggagtc actgatgtac ttttcaactc tttccatttc agcaggatcc 480

<210> 228
 <211> 154
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (12)
 <223> XAA = ANYTHING

<400> 228
 Glu Phe Ala Ala Ala Ser Thr Phe Phe Phe Phe Xaa Phe Phe Phe Phe
 1 5 10 15
 Phe Phe Phe Phe Phe Lys Asn Asn Thr Tyr Val Val Cys Thr Gly His
 20 25 30
 Lys Gly Met Gly Pro Leu Val Asn Pro Leu Leu Gly His Asp Thr Ser
 35 40 45
 Thr Ser Ile Ser Pro Glu Ser Val Cys Cys Glu Leu Pro Leu Gly Gly
 50 55 60
 Ser Gly Leu Val Ser Glu Pro Leu Cys Pro Ser Ile Gly Pro Leu Cys
 65 70 75 80
 Ser Leu Pro Val Phe Ala Leu Ser Ser Gly Ala Ser Thr Phe Gly Leu
 85 90 95
 Gly Leu Thr Met Gly Leu Gln Lys Leu Ser Ser Ser Phe Asp Phe Val
 100 105 110
 Thr Ile Ser Asp Thr Phe Thr Thr Gly Ser Val Arg Leu Asn Leu Phe
 115 120 125
 Cys Ala Phe Ile Leu Leu Phe Ser Gln Phe Met Glu Ser Leu Met Tyr
 130 135 140
 Phe Ser Thr Leu Ser Ile Ser Ala Gly Ser
 145 150

<210> 229
 <211> 420
 <212> DNA
 <213> Mus musculus

<400> 229
 gaattcgcg cgcgctcgac tttttttttt tttttttttt tttttttttt tttttttttt 60
 ttttgatttt tccaagataa aactttattg gagacagcaa ggagtatact gaaagtgggg 120
 gagccatgcc ttcatcccat aactgcaatc agatgctctc ctctgagaga gagtgtgtgg 180
 ggagccaagg tgagaagcag gtatgattca caccccaact gcttggagag tgcttatatg 240
 acagtctttt tctcgatttt attttttctc agttcttcaa cacacacttt ggcttcattt 300

gggggaaaat taaacaaaag aacagaattt ccttccccca gagttactta tgaaatgaca 360
cagctgccct tttctttgaa gggattcttg tcttctggga ttccctttac cagaggatcc 420

<210> 230

<211> 139

<212> PRT

<213> Mus musculus

<400> 230

Glu Phe Ala Ala Ala Ser Thr Phe Phe Phe Phe Phe Phe Phe Phe Phe
1 5 10 15

Phe Phe Phe Phe Phe Phe Phe Gln Asp Lys Thr Leu Leu Glu Thr Ala
20 25 30

Arg Ser Ile Leu Lys Val Gly Glu Pro Cys Leu His Ser Ile Thr Ala
35 40 45

Ile Arg Cys Ser Pro Leu Arg Glu Ser Val Trp Gly Ala Lys Val Arg
50 55 60

Ser Arg Tyr Asp Ser His Pro Asn Cys Leu Glu Ser Ala Tyr Met Thr
65 70 75 80

Val Phe Phe Ser Ile Leu Phe Phe Leu Ser Ser Ser Thr His Thr Leu
85 90 95

Ala Ser Phe Gly Gly Lys Leu Asn Lys Arg Thr Glu Phe Pro Ser Pro
100 105 110

Arg Val Thr Tyr Glu Met Thr Gln Leu Pro Phe Ser Leu Lys Gly Phe
115 120 125

Leu Ser Ser Gly Ile Pro Phe Thr Arg Gly Ser
130 135

<210> 231

<211> 629

<212> DNA

<213> Mus musculus

<400> 231

gaattcgagg ccgcgtcgac gtcactgtgg agctcagatc acagtgtctga cagaatccat 60
atttgagaaa ttacataagg tttgaaagag aggatagtga aaggatacga attcctaaaa 120
acgttttaac tggccttttg tttgaacgaa agagaaaattg aaaccaaattg aaataaatta 180
cttgtagaaa agaatactgc caacagcata gcaaaatgaa attcttctctg ctgctttccc 240
tcattggatt ctgctggggc caatatgacc cacatactca atatggacga actgctattg 300
tccacctgtt tgagtggcgc tgggttgata ttgctaagga atgtgagaga tacttagctc 360
ctaattggatt tgcaggtgtg caggtctctc caccatga aaacatcgta gtccacagcc 420
cttcaagacc atgggtgggaa agatatcaac caattagcta caaaatatgt tccaggtctg 480
gaaatgaaga tgaattcagg gacatggtga acaggtgcaa caatgttggg gtccgtatctt 540
atgtggatgc tgtcattaac cacatgtgtg gagggtgggc tcaagctgga caaagcagta 600
catgtggaag ttatttcaac cccgatcc 629

<210> 232
 <211> 204
 <212> PRT
 <213> Mus musculus

<400> 232
 Ile Arg Gly Arg Val Asp Val Thr Val Glu Leu Arg Ser Gln Cys Gln
 1 5 10 15
 Asn Pro Tyr Leu Glu Asn Tyr Ile Arg Phe Glu Arg Glu Asp Ser Glu
 20 25 30
 Arg Ile Arg Ile Pro Lys Asn Val Ser Gly Leu Leu Phe Glu Arg Lys
 35 40 45
 Arg Asn Asn Gln Met Lys Ile Thr Cys Lys Glu Tyr Cys Gln Gln His
 50 55 60
 Ser Lys Met Lys Phe Phe Leu Leu Leu Ser Leu Ile Gly Phe Cys Trp
 65 70 75 80
 Ala Gln Tyr Asp Pro His Thr Gln Tyr Gly Arg Thr Ala Ile Val His
 85 90 95
 Leu Phe Glu Trp Arg Trp Val Asp Ile Ala Lys Glu Cys Glu Arg Tyr
 100 105 110
 Leu Ala Pro Asn Gly Phe Ala Gly Val Gln Val Ser Pro Pro Asn Glu
 115 120 125
 Asn Ile Val Val His Ser Pro Ser Arg Pro Trp Trp Glu Arg Tyr Gln
 130 135 140
 Pro Ile Ser Tyr Lys Ile Cys Ser Arg Ser Gly Asn Glu Asp Glu Phe
 145 150 155 160
 Arg Asp Met Val Asn Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val
 165 170 175
 Asp Ala Val Ile Asn His Met Cys Gly Val Gly Ala Gln Ala Gly Gln
 180 185 190
 Ser Ser Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser
 195 200

<210> 233
 <211> 254
 <212> DNA
 <213> Mus musculus

<400> 233
 gaattcgcgg ccgcgtcgac ggatttttct tgagaaaatc ttgggtgaga ttattctgga 60

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ttctatttaa atgtgtgtat ataatgatta ggattttatt tttacagtca tatctacttc 120
cttccttatg tgcgaaatct attgcaacat attatgcacc atactcaaat ccctgggtgtt 180
ccagccaagg ttcttgggtt tcaccacagt acagtaatgt gactccaata ccagaaggaa 240
agaatgtggg atcc 254

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<210> 234
<211> 84
<212> PRT
<213> Mus musculus

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<400> 234
Ile Arg Gly Arg Val Asp Gly Phe Phe Leu Arg Lys Ser Trp Val Arg
 1             5             10             15

Leu Phe Trp Ile Leu Phe Lys Cys Val Tyr Ile Met Ile Arg Ile Leu
      20             25             30

Phe Leu Gln Ser Tyr Leu Leu Pro Ser Leu Cys Ala Lys Ser Ile Ala
      35             40             45

Thr Tyr Tyr Ala Pro Tyr Ser Asn Pro Trp Cys Ser Ser Gln Gly Ser
      50             55             60

Trp Val Ser Pro Gln Tyr Ser Asn Val Thr Pro Ile Pro Glu Gly Lys
      65             70             75             80

Asn Val Gly Ser

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<210> 235
<211> 660
<212> DNA
<213> Mus musculus

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<220>
<221> modified_base
<222> (10)..(166)
<223> N = A, C, G OR T/U

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<400> 235
gtcacccaan actgcggcat tatgaggaca ttatgacgaa ataaggttaa aaaagaagtg 60
aagaacagtt ggggccagtg gcgaaganac acggccaggn tggcaaaaana gtgcagcggc 120
acaggccgat tggaaaccgac atgaggatct acgcaaccga ctcggncagt accgcaacga 180
ggtgcacacc atgctgggac agagcacaga gaagatacgg gcgcggctct ccacacacct 240
gcgcaagatg cgcaagcgtt tgatgcggga tgccgaggat ctgcagaagc gcctagctgt 300
gtacaagcag gggcacgcga gggcgccgag cgcggtgtga gtgccatccg tgagcgcctg 360
gggcctcttg tggagcaagg tcgccagcgc accgccaacc taggcgctgg ggccgcccag 420
cctctgcgcg atcgcgccca ggcttttggg gaccgcatcc gagggcggct ggaggaagtg 480
ggcaaccagg ccgctgaccg cctagaggag gtgcgtgagc acatggagga ggtgcgctcc 540
aagatggagg aactctcgag tcccagcatc agagcgcgtg gaccttttcc cgcgctcccgc 600
agcatgcagg tctcccgtgt gctggccgcg ctgtgcggca tgctactctg cgccggatcc 660

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<210> 236
 <211> 218
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (4)..(54)
 <223> XAA = ANYTHING

<400> 236

Val	Thr	Gln	Xaa	Cys	Gly	Ile	Met	Arg	Thr	Leu	Arg	Asn	Lys	Val	Lys
1				5					10					15	
Lys	Glu	Val	Lys	Asn	Ser	Trp	Val	Gln	Trp	Arg	Arg	Xaa	Thr	Ala	Arg
			20					25					30		
Xaa	Ala	Lys	Xaa	Cys	Ser	Gly	Thr	Gly	Arg	Leu	Glu	Pro	Thr	Gly	Ser
		35					40					45			
Thr	Gln	Pro	Thr	Arg	Xaa	Val	Pro	Gln	Arg	Gly	Ala	His	His	Ala	Gly
	50					55					60				
Pro	Glu	His	Arg	Glu	Asp	Thr	Gly	Ala	Ala	Leu	His	Thr	Pro	Ala	Gln
65					70					75					80
Asp	Ala	Gln	Ala	Leu	Asp	Ala	Gly	Cys	Arg	Gly	Ser	Ala	Glu	Ala	Pro
				85					90					95	
Ser	Cys	Val	Gln	Ala	Gly	Ala	Arg	Glu	Gly	Ala	Glu	Arg	Gly	Val	Ser
			100					105					110		
Ala	Ile	Arg	Glu	Arg	Leu	Gly	Pro	Leu	Val	Glu	Gln	Gly	Arg	Gln	Arg
			115				120					125			
Thr	Ala	Asn	Leu	Gly	Ala	Gly	Ala	Ala	Gln	Pro	Leu	Arg	Asp	Arg	Ala
			130			135					140				
Gln	Ala	Phe	Gly	Asp	Arg	Ile	Arg	Gly	Arg	Leu	Glu	Glu	Val	Gly	Asn
145					150					155					160
Gln	Ala	Arg	Asp	Arg	Leu	Glu	Glu	Val	Arg	Glu	His	Met	Glu	Glu	Val
				165					170					175	
Arg	Ser	Lys	Met	Glu	Glu	Leu	Ser	Ser	Pro	Ser	Ile	Arg	Ala	Arg	Gly
			180					185					190		
Pro	Phe	Pro	Ala	Ser	Arg	Ser	Met	Gln	Val	Ser	Arg	Val	Leu	Ala	Ala
			195				200					205			
Leu	Cys	Gly	Met	Leu	Leu	Cys	Ala	Gly	Ser						
	210					215									

<210> 237

<211> 519
 <212> DNA
 <213> Mus musculus

<400> 237
 cctgcaggag atatatccag agctgcagat cacaaatgtg atgaagcaaa ccagccagtc 60
 aatattgata gttggtgccg aagggacaaa aggcagtgcg agagtcacat tgttatacca 120
 ttcaagtgtc ttgtgggtga atttgtaagt gatgtcctgc tagttccaga taactgccag 180
 tttttccacc aagagcggat ggaggtgtgt gagaagcacc agcgctggca cacgttagtc 240
 aaggaggcat gtctgactga ggggctgacc ttatatagct atggcatgct gctgccctgc 300
 ggggtagacc agttccatgg caccgagtat gtgtgctgcc ctcagacaaa gactgttgac 360
 tcggactcga ctatgtccaa agaagaggag gaagaggaag aggatgaaga ggacgaagag 420
 gaagactatg atcttgataa aagtgaattt cctactgaag cagatttgga agacttcaca 480
 gaagcagcag cagatgagga agaagaggat gaggggatcc 519

<210> 238
 <211> 173
 <212> PRT
 <213> Mus musculus

<400> 238
 Pro Ala Gly Asp Ile Ser Arg Ala Ala Asp His Lys Cys Asp Glu Ala
 1 5 10 15
 Asn Gln Pro Val Asn Ile Asp Ser Trp Cys Arg Arg Asp Lys Arg Gln
 20 25 30
 Cys Lys Ser His Ile Val Ile Pro Phe Lys Cys Leu Val Gly Glu Phe
 35 40 45
 Val Ser Asp Val Leu Leu Val Pro Asp Asn Cys Gln Phe Phe His Gln
 50 55 60
 Glu Arg Met Glu Val Cys Glu Lys His Gln Arg Trp His Thr Leu Val
 65 70 75 80
 Lys Glu Ala Cys Leu Thr Glu Gly Leu Thr Leu Tyr Ser Tyr Gly Met
 85 90 95
 Leu Leu Pro Cys Gly Val Asp Gln Phe His Gly Thr Glu Tyr Val Cys
 100 105 110
 Cys Pro Gln Thr Lys Thr Val Asp Ser Asp Ser Thr Met Ser Lys Glu
 115 120 125
 Glu Glu Glu Glu Glu Glu Asp Glu Glu Asp Glu Glu Glu Asp Tyr Asp
 130 135 140
 Leu Asp Lys Ser Glu Phe Pro Thr Glu Ala Asp Leu Glu Asp Phe Thr
 145 150 155 160
 Glu Ala Ala Ala Asp Glu Glu Glu Glu Asp Glu Gly Ser
 165 170

<210> 239
 <211> 678
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (9)..(160)
 <223> N = A, C, G OR T/U

<400> 239
 gtggcccant ccggcccntg cccagtgngt ggctccngct ggcacgccag cggccttggg 60
 agaagctcaa gcccagtagg ccggcgcgcc ntgccgccgg tgcaaaagag acggagctcc 120
 cggcccccg cgggtggagcg ggggatcaat gcggttcagn aatcgattcc agcgtttcat 180
 gaaccatcgg gcccagtaa tggccgctac aaaccaacgt gctacgaaca tgctgccaat 240
 tgctacacac acgcattcct cattgttccg gccattgtgg gcagtgccct cctccatcgg 300
 ctgtctgatg actgctggga gaagataaca gcatggatct acgggatggg cctttgtgcc 360
 ctcttcacg tctccacagt gtttcacata gtatcatgga agaagagcca cttgagaaca 420
 gtggagcatt gttccacat gtgcgacgg atggcatct acttcttcat tgctgcttcc 480
 tacgccccat gggttaaact cctgaactt ggaccctgg catctcatat gcgttggttt 540
 atctggctca tggcagctgg aggaaccatt tatgtatttc tctaccatga aaagtataaa 600
 gtggttgaac ttttcttcta tctcacgat ggattttctc cagccttggg ggtgacatca 660
 atgaataaca ctggatcc 678

<210> 240
 <211> 225
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (3)..(53)
 <223> XAA = ANYTHING

<400> 240
 Val Ala Xaa Ser Gly Pro Cys Pro Val Xaa Gly Ser Xaa Trp His Ala
 1 5 10 15
 Ser Gly Leu Gly Arg Ser Ser Ser Pro Gly Arg Arg Ala Xaa Pro Pro
 20 25 30
 Val Gln Lys Arg Arg Ser Ser Arg Pro Pro Arg Val Glu Arg Gly Ile
 35 40 45
 Asn Ala Val Gln Xaa Ser Ile Pro Ala Phe His Glu Pro Ser Gly Pro
 50 55 60
 Ser Asn Gly Arg Tyr Lys Pro Thr Cys Tyr Glu His Ala Ala Asn Cys
 65 70 75 80
 Tyr Thr His Ala Phe Leu Ile Val Pro Ala Ile Val Gly Ser Ala Leu
 85 90 95

Leu His Arg Leu Ser Asp Asp Cys Trp Glu Lys Ile Thr Ala Trp Ile
 100 105 110

Tyr Gly Met Gly Leu Cys Ala Leu Phe Ile Val Ser Thr Val Phe His
 115 120 125

Ile Val Ser Trp Lys Lys Ser His Leu Arg Thr Val Glu His Cys Phe
 130 135 140

His Met Cys Asp Arg Met Val Ile Tyr Phe Phe Ile Ala Ala Ser Tyr
 145 150 155 160

Ala Pro Trp Leu Asn Leu Arg Glu Leu Gly Pro Leu Ala Ser His Met
 165 170 175

Arg Trp Phe Ile Trp Leu Met Ala Ala Gly Gly Thr Ile Tyr Val Phe
 180 185 190

Leu Tyr His Glu Lys Tyr Lys Val Val Glu Leu Phe Phe Tyr Leu Thr
 195 200 205

Met Gly Phe Ser Pro Ala Leu Val Val Thr Ser Met Asn Asn Thr Gly
 210 215 220

Ser
 225

<210> 241
 <211> 655
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified base
 <222> (16)..(85)
 <223> N = A, C, G OR T/U

<400> 241
 gttgtagatc tgaaancaag aaagaaggcg gggcttgagg tcctgaggtc acttaagggc 60
 cacntnttt gacntaagac ctcantaggc cccgcctcta aaggtttctg acctcaatag 120
 gccttctctg agaactagtt tctaactctc aggcccttgg gacattgcat ctgagtagta 180
 ggtgcctctc tacctgtgtt tggcttggtc atgattggca gacactctgc ctggctctgc 240
 acagcagcgg ctcagcatca gcatccagct gcttgctgtg tgtagttgt ctcacagctg 300
 agggctctgc ctggctact tcaggctttc cggttaggaa gataatttg tcaactgtgt 360
 ctgtggccac tcttagaatt ttctcttttg agggaacctg tgactgggtg gcttttgcat 420
 tctatggagg gagatggggt taaagactgt ggcaacacac accctccaga agagctggga 480
 ccagagactg tcagcacaga aaggacaatg tcttttttag tagctgtggc agacttgagt 540
 tgctgtaatt tatacaaat gtttagaatg gtttttaaga ctaagaagg aaatatactt 600
 attgcacaag acttttataa ttactatact taaattatgc tctatgtggg gatcc 655

<210> 242
 <211> 201
 <212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (3)..(25)

<223> XAA = ANYTHING

<400> 242

Leu Ile Xaa Gln Glu Arg Arg Arg Gly Leu Arg Ser Gly His Leu Arg
1 5 10 15

Ala Thr Xaa Phe Asp Xaa Arg Pro Xaa Ala Pro Pro Leu Lys Val Ser
20 25 30

Asp Leu Asn Arg Pro Ser Trp Arg Thr Ser Phe Leu Ser Gly Pro Trp
35 40 45

Asp Ile Ala Ser Gln Val Pro Leu Tyr Leu Cys Leu Ala Cys Ser Leu
50 55 60

Ala Asp Thr Leu Pro Gly Ser Ala Gln Gln Arg Leu Ser Ile Ser Ile
65 70 75 80

Gln Leu Leu Ala Val Cys Leu Ser His Ser Gly Leu Cys Leu Gly Tyr
85 90 95

Phe Arg Leu Ser Gly Glu Asp Asn Leu Val Thr Cys Val Cys Gly His
100 105 110

Ser Asn Phe Leu Phe Gly Asn Leu Leu Val Gly Phe Cys Ile Leu Trp
115 120 125

Arg Glu Met Gly Leu Lys Thr Val Ala Thr His Thr Leu Gln Lys Ser
130 135 140

Trp Asp Gln Arg Leu Ser Ala Gln Lys Gly Gln Cys Leu Phe Leu Trp
145 150 155 160

Gln Thr Val Ala Val Ile Tyr Thr Asn Cys Leu Glu Trp Phe Leu Arg
165 170 175

Leu Arg Arg Glu Ile Tyr Leu Leu His Lys Thr Phe Ile Ile Thr Ile
180 185 190

Leu Lys Leu Cys Ser Met Trp Gly Ser
195 200

<210> 243

<211> 677

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (1)

<223> N = A, C, G OR T/U

<400> 243

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ncgctgtagt ttcattttctc acttttgaggg cacagatgaa aatgtatatc gcaacacagt 60
ggatatcagc ccaagcacga agaccatgct gaacatgcac ccgtacagag tgtacttaaa 120
ggagtcgtca taagggcact gggagccatt ggagcttacc attgtcaggc agtgcagctt 180
acaggaggcc ttttgtccgc agcgcttgat cgatcgccctt tgctattcag atgtgggtcac 240
agcagcagcc agtttatattg caaagtatatt gtttcttttc ctgttcttac aaatactttc 300
ttctcttaac tcttcaaagg aaacatgaaa tgtgttccgt aaaagtttct agtagattat 360
tcaggaaaaat agtctgattt tctggctcag aaaatccatg agtctggagt ttagttaact 420
gacagaaaaat gcagtcgaagg aagccaaccc ataaagctga aagtgtgaagg aaaaactgtt 480
ccaagtcgga ccagaccagt ccgcgtggaa acttgtgctt cagccgccag ggtccaaacc 540
agctttactt cagtcacaaa cactcgccgt gcgtccgtcc gcccgctcgtc ctcgggtact 600
tcttccttct ttttattctc aaactttgta tttctacatt gattccggac ggcgataggc 660
agtcgtttaa gggatcc 677
```

<210> 244

<211> 219

<212> PRT

<213> Mus musculus

<400> 244

```
Ala Val Val Ser Phe Leu Thr Leu Arg Ala Gln Met Lys Met Tyr Ile
  1              5              10              15

Ala Thr Gln Trp Ile Ser Ala Gln Ala Arg Arg Pro Cys Thr Cys Thr
      20              25              30

Arg Thr Glu Cys Thr Arg Ser Arg His Lys Gly Thr Gly Ser His Trp
      35              40              45

Ser Leu Pro Leu Ser Gly Ser Ala Ala Tyr Arg Arg Pro Phe Val Arg
      50              55              60

Ser Ala Ser Ile Ala Phe Ala Ile Gln Met Trp Ser Gln Gln Gln Pro
      65              70              75              80

Val Tyr Leu Gln Ser Ile Cys Phe Phe Ser Cys Ser Tyr Lys Tyr Phe
      85              90              95

Leu Leu Leu Thr Leu Gln Arg Lys His Glu Met Cys Ser Val Lys Val
      100             105             110

Ser Ser Arg Leu Phe Arg Lys Ile Val Phe Ser Gly Arg Glu Asn Pro
      115             120             125

Val Trp Ser Leu Val Asn Gln Lys Met Gln Ser Arg Lys Pro Thr His
      130             135             140

Lys Ala Glu Ser Val Arg Lys Asn Cys Ser Lys Ser Asp Gln Thr Ser
      145             150             155             160

Pro Arg Gly Asn Leu Cys Phe Ser Arg Gln Gly Pro Asn Gln Leu Tyr
```


165

170

175

Phe Ser His Lys His Ser Pro Cys Val Arg Pro Pro Val Val Leu Gly
 180 185 190

Tyr Phe Phe Leu Leu Phe Ile Leu Lys Leu Cys Ile Ser Thr Leu Ile
 195 200 205

Pro Asp Gly Asp Arg Gln Ser Phe Lys Gly Ser
 210 215

<210> 245

<211> 660

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (7)..(45)

<223> N = A, C, G OR T/U

<400> 245

agagatncaa tctaaaaagc agatantgag cagagactan ggagnagtta acatactaaa 60
 ccgctacata cataggacaa atgccatttg gaggctgaag tcaaggaaac atcagtatac 120
 atgtaagttt ggcattgtat ttgggtgcga ttaaattggaa agggcttttg tactgagttg 180
 agatcttata tcctagataa tagagtgtat tgggtttgaa taggaagtgt catggacaga 240
 gctctgagcc tgtaggagca aggagtatca caaaggctct ttgccacagc ccaggcaagc 300
 aatctagagc ttaagcctag ggtggcagat gtgtggaaga acacagacac agttgtgcag 360
 agcctgggaa acggcttggg cttccagga agaggtttat gttatcgttg tttgggttgg 420
 gttgtttatt tctgggggct gggggaggga aggtatgtat gttttgttgt ttagtatctc 480
 atgtagccag gatggccttg aactcactat gtagctcaga ctgacgtgga attccaggtt 540
 ctctctttac tccccacact ggtagctgtg caccataaaa cctggcttat actttgtaaa 600
 atcccaatat tctcttgctt gctttcagca cccttatcac atgtgtggat tctgggatcc 660

<210> 246

<211> 211

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (3)..(14)

<223> XAA = ANYTHING

<400> 246

Arg Asp Xaa Ile Lys Ala Asp Xaa Glu Gln Arg Leu Xaa Xaa Ser His
 1 5 10 15

Thr Lys Pro Leu His Thr Asp Lys Cys His Leu Glu Ala Glu Val Lys
 20 25 30

Glu Thr Ser Val Tyr Met Val Trp His Cys Ile Trp Leu Arg Leu Asn
 35 40 45

Gly Lys Gly Phe Cys Thr Glu Leu Arg Ser Tyr Leu Leu Asp Asn Arg
 50 55 60
 Val Tyr Trp Val Ile Gly Ser Val Met Asp Arg Ala Leu Ser Leu Glu
 65 70 75 80
 Gln Gly Val Ser Gln Arg Leu Phe Ala Thr Ala Gln Ala Ser Asn Leu
 85 90 95
 Glu Leu Lys Pro Arg Val Ala Asp Val Trp Lys Asn Thr Asp Thr Val
 100 105 110
 Val Gln Ser Leu Gly Asn Gly Leu Gly Phe Gln Gly Arg Gly Leu Cys
 115 120 125
 Tyr Arg Cys Leu Gly Trp Val Val Tyr Phe Trp Gly Leu Gly Glu Gly
 130 135 140
 Arg Tyr Val Cys Phe Val Val Tyr Leu Met Pro Gly Trp Pro Thr His
 145 150 155 160
 Tyr Val Ala Gln Thr Asp Val Glu Phe Gln Val Leu Ser Leu Leu Pro
 165 170 175
 Thr Leu Val Ala Val His His Lys Thr Trp Leu Ile Leu Cys Lys Ile
 180 185 190
 Pro Ile Phe Ser Cys Leu Leu Ser Ala Pro Leu Ser His Val Trp Ile
 195 200 205
 Leu Gly Ser
 210

<210> 247

<211> 673

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (4)..(173)

<223> N = A, C, G, OR T/U

<400> 247

gttnnnnncc nttnnnnnna antntntnnn aatnaaaaag nanantaann nnanntnnnn 60
 ncngnttnnn ccccnnttcc nnnnnnctan gnnncnggct tnannntggn gttantngnn 120
 ntggtaatac nngggggccaa gcntgcntgt gtaaagcaag nccctnantg agnttctcct 180
 catcagcggg gttcagacct ggctgggttg taggtacact agccacgatc agcacaagtc 240
 acaagtgccca ctcaattaca cccatcccc cagcctaataa ctttctccta aggtgccaag 300
 ggatcagtcga gtctgaagga tgaaaaccag agcgtgggtg acagctctcc cttcaaact 360
 gaagccaccc tgggggacgg gggatatcgt atcccacgtt taaccataaa tagggctctg 420
 atgaaaaggg ggaaggaaaa aaagactact ctaacagcaa atttttcttt ttaggttta 480
 aaactcttgc taaaattcct agtgaatcag tgcttttgaa taaaagtatc ataagccaat 540

```
gccacaggta tcatacgcta atgtcagggg ggtgctatgg gtgtcctttt gttgctgttt 600
tggtctgttt tctttcctat gtcaatgtgg cttcacaagt gtgggatttc aagaggtgaa 660
gatacatgga tcc 673
```

```
<210> 248
<211> 210
<212> PRT
<213> Mus musculus
```

```
<220>
<221> MOD_RES
<222> (1)..(56)
<223> XAA = ANYTHING
```

```
<400> 248
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Lys Xaa Xaa Xaa
 1             5             10             15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Phe Xaa Xaa Xaa Xaa Xaa
 20             25             30
Ala Xaa Xaa Trp Xaa Xaa Xaa Xaa Trp Tyr Xaa Gly Pro Ser Xaa Xaa
 35             40             45
Val Ser Lys Xaa Leu Xaa Glu Xaa Leu Leu Ile Ser Gly Val Gln Thr
 50             55             60
Trp Leu Val Cys Arg Tyr Thr Ser His Asp Gln His Lys Ser Gln Val
 65             70             75             80
Pro Leu Thr Tyr Thr His Pro Pro Ser Leu Lys Leu Ser Pro Lys Val
 85             90             95
Pro Arg Asp Gln Ser Val Arg Met Lys Thr Arg Ala Trp Cys Thr Ala
100             105             110
Leu Pro Phe Lys Leu Lys Pro Pro Trp Gly Thr Gly Val Ser Leu Ser
115             120             125
His Val Pro Ile Gly Ser Lys Gly Gly Arg Lys Lys Arg Leu Leu Gln
130             135             140
Gln Ile Phe Leu Phe Val Asn Ser Cys Asn Ser Ile Ser Ala Leu Glu
145             150             155             160
Lys Tyr His Lys Pro Met Pro Gln Val Ser Tyr Ala Asn Val Arg Glu
165             170             175
Val Leu Trp Val Ser Phe Cys Cys Cys Phe Val Leu Phe Ser Phe Leu
180             185             190
Cys Gln Cys Gly Phe Thr Ser Val Gly Phe Gln Glu Val Lys Ile His
195             200             205
```

Gly Ser
210

<210> 249
<211> 656
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (2)..(68)
<223> N = A, C, G OR T/U

<400> 249
anaattcgcg ncggcgtcga cgcctaacca aaaacacagg tcagttttgg agaccctcac 60
acagatcntg gaatgagatc tgcagccagg tgtccagccc aggcttgggc ttctcattgt 120
acccaaggct ggaagggttt ggtctgtact aacacacaag ctcgcagtcc tgcttgactg 180
ctggcttccc aaagaggaga cattgggtctt gctgggaggc acagcaggag agtgaccac 240
tgccactgca ctctaactga gtactaaggc cactagggtt ttctagacct cgctttcccc 300
ttgagcttcc tggggagggtg aagtgagggtg tgtgtgtgtg tgtgtgtctt tgtgtgctta 360
gatttattgc agggaaagggt ctaatccaga atcagtattc aggctttgtc atgttgatc 420
agtgcccaagg tgaccctcaa ggatcatgtaa ctttaagcaa gcttagcatt tattttattc 480
ctgaaaactt aagtatttta cttttttgtg tgttcgtgga gacatttgca gtattaatga 540
ttttattttt cctaaatcgg gatggaaaca aacttttcca ggttatgtta ataagccact 600
taagtgcctt aaacagcttt ggtgtagatg agaattgctg ggtccgtcat ggatcc 656

<210> 250
<211> 214
<212> PRT
<213> Mus musculus

<400> 250
Asn Ser Arg Arg Arg Arg Leu Thr Lys Asn Thr Gly Gln Phe Trp
1 5 10 15
Arg Pro Ser His Arg Ser Trp Asn Glu Ile Cys Ser Gln Val Ser Ser
20 25 30
Pro Gly Leu Gly Phe Ser Leu Tyr Pro Arg Leu Glu Gly Phe Gly Leu
35 40 45
Tyr His Thr Ser Ser Gln Ser Cys Leu Thr Ala Gly Phe Pro Lys Arg
50 55 60
Arg His Trp Ser Cys Trp Glu Ala Gln Gln Glu Ser Asp Pro Leu Pro
65 70 75 80
Leu His Ser Asn Val Leu Arg Pro Leu Gly Leu Ser Arg Pro Arg Phe
85 90 95
Pro Leu Glu Leu Pro Gly Glu Val Lys Gly Val Cys Val Cys Val Cys
100 105 110

Leu Cys Val Leu Arg Phe Ile Ala Gly Lys Gly Leu Ile Gln Asn Gln
 115 120 125
 Tyr Ser Gly Phe Val Met Leu Tyr Gln Cys Gln Gly Asp Pro Gln Gly
 130 135 140
 His Val Thr Ala Lys Leu Ser Ile Tyr Phe Ile Pro Glu Asn Leu Ser
 145 150 155 160
 Ile Leu Leu Phe Cys Val Phe Val Glu Thr Phe Ala Val Leu Met Ile
 165 170 175
 Leu Phe Phe Leu Asn Arg Asp Gly Asn Lys Leu Phe Gln Val Met Leu
 180 185 190
 Ile Ser His Leu Ser Ala Leu Asn Ser Phe Gly Val Asp Glu Asn Cys
 195 200 205
 Trp Val Arg His Gly Ser
 210

<210> 251
 <211> 372
 <212> DNA
 <213> Mus musculus

<400> 251
 gaattcgcg cgcgctcgac acagctttta acccccatg ctactgttaa gggtggggcg 60
 ctctgtgaaa tccacacttg gcctcccaag agcttcctca cagcctggta agccttacac 120
 tcgggtgaga tgagatgata tttgtgttta ctggtgcttc gtttttcttt atgggtcgct 180
 tagaatttgt cccactctgt ttgtagtgtt ggctgtactg atgtggaaga gaaagttatg 240
 cagtctcaat cttcttatgc acagcatctc tgcctgactt tgtggtgcct ctgttttgtg 300
 cacatgcaca tgtgttcagt gttggcattg ggaatggcta tgtgcttcac caccgcttag 360
 gcctggggat cc 372

<210> 252
 <211> 211
 <212> PRT
 <213> Mus musculus

<400> 252
 Gly Gln Gly Ala His Ala Gly Arg Gly Gly Ser Ser Ser Pro Met Ala
 1 5 10 15
 Met Pro Ala Cys Arg Ile Ser Trp Lys Trp Pro Leu Phe Trp Ile His
 20 25 30
 Arg Leu Cys Arg Leu Gly Gly Arg Thr Ala Ile Arg Thr Arg Trp Leu
 35 40 45
 Pro Val Ile Leu Arg Ala Trp Arg Arg Met Gly Pro Leu Pro Arg Ala
 50 55 60

Leu Arg Tyr Arg Arg Ser Arg Phe Ala Ala His Arg Leu Leu Ser Pro
 65 70 75 80
 Ser Arg Val Leu Leu Asn Lys Arg Lys Ser Lys Leu Glu Phe Ala Ala
 85 90 95
 Ala Ser Thr Gln Leu Thr Pro His Ala His Cys Lys Val Gly Ala Leu
 100 105 110
 Cys Glu Ile His Thr Trp Pro Pro Lys Ser Phe Leu Thr Ala Trp Ala
 115 120 125
 Leu His Ser Gly Glu Met Arg Tyr Leu Cys Leu Leu Val Leu Arg Phe
 130 135 140
 Ser Leu Trp Val Ala Asn Leu Ser His Ser Val Cys Ser Ala Gly Cys
 145 150 155 160
 Thr Asp Val Glu Glu Lys Val Met Gln Ser Gln Ser Ser Tyr Ala Gln
 165 170 175
 His Leu Cys Leu Thr Leu Trp Cys Leu Cys Phe Val His Met His Met
 180 185 190
 Cys Ser Val Leu Ala Leu Gly Met Ala Met Cys Phe Thr Thr Ala Ala
 195 200 205
 Trp Gly Ser
 210

<210> 253

<211> 689

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (62)..(85)

<223> N = A, C, G OR T/U

<400> 253

aggtaagtag tgttgactta cattaagcgc ctacatcgat ttctttcatt gaagaatata 60
 cntctagtga tttttacctg gggcnttttt tgagagtgag ggtatagggtg acaggtagga 120
 ggagtggctg tgataagggt gactgctggt cctcctgaag ctattgatca tgccccaaga 180
 agctgatgac caccatgtgt cattgaatat aaaccttggg gtttagtgag acttttgaag 240
 ttaattccaa tttacctaac agactttgga tttgaagaga ctttaaactt gtctcttatt 300
 acttttgtgt tttgatgtct tttcagtaat gtatcttttg tgagttaccc tagttacaaa 360
 gtacctgagt aacagagtag cttcgagaca gagtacccta gtaacagagt accctagtaa 420
 cagagtaccc tagagacagt acctcagtga cagagtaccc tagtgacaga tgaccctagt 480
 gacaggttac ctagttagag gttaccctga tgacattggt atgttatctt tgaagataaa 540
 atagttctgt gctacatgtc tttaaataat aggttaagaa ttgttctaga aatttacata 600
 atgatttgca tagattagct cccatctttg ttttattcct ttgttggttg tttgagagaa 660
 gctttctgct acatcgccag agcggatcc 689

<210> 254
 <211> 209
 <212> PRT
 <213> Mus musculus

<400> 254

Val Ser Ser Val Asp Leu His Ala Pro Thr Ser Ile Ser Phe Ile Glu
 1 5 10 15

Glu Tyr Thr Ser Ser Asp Phe Tyr Leu Gly Xaa Phe Leu Arg Val Arg
 20 25 30

Val Val Thr Gly Arg Arg Ser Gly Cys Asp Lys Gly Asp Cys Trp Ser
 35 40 45

Ser Ser Tyr Ser Cys Pro Lys Lys Leu Met Thr Thr Met Cys His Ile
 50 55 60

Thr Leu Gly Phe Ser Glu Thr Phe Glu Val Asn Ser Asn Leu Pro Asn
 65 70 75 80

Arg Leu Trp Ile Arg Asp Phe Lys Ser Val Ser Tyr Tyr Phe Cys Val
 85 90 95

Leu Met Ser Phe Gln Cys Ile Phe Cys Glu Leu Pro Leu Gln Ser Thr
 100 105 110

Val Thr Glu Tyr Leu Arg Asp Arg Val Pro Gln Ser Thr Leu Val Thr
 115 120 125

Glu Tyr Pro Arg Asp Ser Thr Ser Val Thr Glu Tyr Pro Ser Asp Arg
 130 135 140

Pro Gln Val Thr Leu Gln Val Thr Leu Val Thr Leu Leu Cys Tyr Leu
 145 150 155 160

Arg Asn Ser Ser Val Leu His Val Phe Lys Val Lys Asn Cys Ser Arg
 165 170 175

Asn Leu His Asn Asp Leu His Arg Leu Ala Pro Ile Phe Val Leu Phe
 180 185 190

Leu Cys Cys Leu Phe Glu Arg Ser Phe Leu Leu His Arg Gln Ser Gly
 195 200 205

Ser

<210> 255
 <211> 668
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (41)..(151)
 <223> N = A, C, G OR T/U

<400> 255

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gatcaaagaa ggggccttca agaacctgaa ggacttgcat ncnttgatcc nttgtcanca 60
acaagatcag caaaatcagt ccagaggcat tcaaacctct ngatgaagttg gaaaggcctt 120
acctgtttta gaaccaacta aaggaactgc ntgaaaaaat gccagaact ctccagggaac 180
ttcgtgtcca tgagaatgag atcaccaagc tgcggaaatc cgacttcaat ggactgaaca 240
atgtgcttgt catagaactg ggcggcaacc cactgaaaaa ctctgggatt gaaaacggag 300
ccttccaggg actgaagagt ctctcatata ttctcatctc agacaccaac ataactgcga 360
tccctcaagg tctgcctact tctctcactg aagtgcactc agatggcaac aagatcacca 420
agggtgatgc acccagcctg aaaggactga ttaatttgtc taaactggga ttgagcttca 480
acagcatcac cggtatggag aatggcagtc tggccaatgt tcctcatctg agggaaactcc 540
acttgacaa caacaaactc ctccaggtgc ctgctgggct ggacagcat aagtatatcc 600
aggctgtcta ccttcacaac aacaacatct ccgcagttgg gcaaaatgac ttctgccaag 660
ctggatcc                                     668

```

<210> 256
 <211> 220
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (12)..(48)
 <223> XAA = ANYTHING

<400> 256

```

Ser Lys Lys Gly Pro Ser Arg Thr Arg Thr Cys Xaa Xaa Ser Xaa Val
  1              5              10              15

Xaa Asn Lys Ile Ser Lys Ile Ser Pro Glu Ala Phe Lys Pro Leu Val
          20              25              30

Lys Leu Glu Arg Leu Tyr Leu Phe Lys Asn Gln Leu Lys Glu Leu Xaa
          35              40              45

Glu Lys Met Pro Arg Thr Leu Gln Glu Leu Arg Val His Glu Asn Glu
          50              55              60

Ile Thr Lys Leu Arg Lys Ser Asp Phe Asn Gly Leu Asn Asn Val Leu
          65              70              75              80

Val Ile Glu Leu Gly Gly Asn Pro Leu Lys Asn Ser Gly Ile Glu Asn
          85              90              95

Gly Ala Phe Gln Gly Leu Lys Ser Leu Ser Tyr Ile Arg Ile Ser Asp
          100              105              110

Thr Asn Ile Thr Ala Ile Pro Gln Gly Leu Pro Thr Ser Leu Thr Glu
          115              120              125

```


Val His Leu Asp Gly Asn Lys Ile Thr Lys Val Asp Ala Pro Ser Leu
 130 135 140

Lys Gly Leu Ile Asn Leu Ser Lys Leu Gly Leu Ser Phe Asn Ser Ile
 145 150 155 160

Thr Val Met Glu Asn Gly Ser Leu Ala Asn Val Pro His Leu Arg Glu
 165 170 175

Leu His Leu Asp Asn Asn Lys Leu Leu Arg Val Pro Ala Gly Leu Ala
 180 185 190

Gln His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser
 195 200 205

Ala Val Gly Gln Asn Asp Phe Cys Gln Ala Gly Ser
 210 215 220

<210> 257
 <211> 692
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (64)..(67)
 <223> N = A, C, G OR T/U

<400> 257
 gactacatag gaaacgaagt ctcgaaatcc aacaataaac tcctcctcct cctcctcctc 60
 ctntntntat ctcttcatat tgtaaagatc ttgtgataaa agtggttttg cttcctggat 120
 tagttttatg ttttaagggtta aacttggttg ttttccctg atttatttct gagcaagttc 180
 attagtatat gtggaaacgt tcctgatttg tgtatgttga aattgtatcc tgttacttta 240
 cccaaagtat ttattatata taggactttt ctagttagatt ttccaagtct tttgcttttg 300
 tgtataggat tacattgtct caaagtaggg ccaattttcc ctgacctttt ctatttttat 360
 cccttttctt tccctgcctt atccctctaa gacatcaagc atcatcctga gtaagaaggg 420
 aagaggacct cttctctcat tcctgctttt cttattgaat gtagcattga ctacagttct 480
 gtcagctata acttttattg tgtaaacgta cattcttttg atgcttggtg cacctgggct 540
 tttatcagga aatgatgttg aaattaataa agaggctctt cctcagctgc tcagacagcc 600
 tctgttgagg tctatctata tgcacctca cgtgtattga tttgtgtatg ttgaatcacc 660
 tgtgcatccc tggaatgaaa gtaactggat cc 692

<210> 258
 <211> 217
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (20)..(21)
 <223> XAA = ANYTHING

<400> 258

Leu His Arg Lys Arg Ser Leu Glu Ile Gln Gln Thr Pro Pro Pro Pro
 1 5 10 15
 Pro Pro Pro Xaa Xaa Ile Ser Ser Tyr Cys Lys Asp Leu Val Ile Lys
 20 25 30
 Val Phe Leu Leu Pro Gly Leu Val Leu Cys Leu Arg Leu Asn Leu Leu
 35 40 45
 Leu Phe Pro Phe Ile Ser Glu Gln Val His Tyr Met Trp Lys Arg Ser
 50 55 60
 Phe Val Tyr Val Glu Ile Val Ser Cys Tyr Phe Thr Gln Ser Ile Tyr
 65 70 75 80
 Tyr Ile Asp Phe Ser Ser Phe Ser Lys Ser Phe Ala Phe Val Tyr Arg
 85 90 95
 Ile Thr Leu Ser Gln Ser Arg Ala Asn Phe Pro Leu Pro Phe Leu Phe
 100 105 110
 Leu Ser Leu Phe Phe Pro Cys Leu Ile Pro Leu Arg His Gln Ala Ser
 115 120 125
 Ser Val Arg Arg Glu Glu Asp Leu Phe Ser His Ser Cys Phe Ser Tyr
 130 135 140
 Met His Leu Gln Phe Cys Gln Leu Leu Leu Leu Cys Arg Thr Phe Phe
 145 150 155 160
 Cys Leu Cys His Leu Gly Phe Tyr Gln Glu Met Met Leu Lys Leu Ile
 165 170 175
 Lys Arg Ser Phe Leu Ser Cys Ser Asp Ser Leu Cys Trp Ser Leu Ser
 180 185 190
 Ile Cys Ile Leu Thr Cys Ile Asp Leu Cys Met Leu Asn His Leu Cys
 195 200 205
 Ile Pro Gly Met Lys Val Thr Gly Ser
 210 215

<210> 259

<211> 705

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (648)

<223> N = A, C, G OR T/U

<400> 259

cttcagcatc ttttactttc accagcgttt ctgggtggga tcccaggggtg cggatctcaa 60

```

gctgggttg agagttggtg ttcaaaccac ggttgtaaac gttaaccacc gctggcgcg 120
cgcggcgaac cgccagatta tagctggcag gcgtctcadc ggtactgtca aattgcggag 180
tggaagcggtg gtttaaggctg cgcagcgaag gcatggcaac cagcagaata gcgccgacaa 240
ttaatccaat cgcaacggaa cgtaagagct tcacaaacat gatggaggcg tcattaaaaa 300
agggaaacggc agcagcatat cagcagttaa cgggacatca cacgtaagcc tgatgcccgg 360
tttacgacat taacgcatca gcagatagat gcttttcattg ccgcgtacaa tttgcagggc 420
gatgatggcc ggttttgccg ccagcacttt acgcatttca gcaatcgagt tcacccgatc 480
gcggttgacg ccaatgatca catcgtcttt ttgcaagcca gcctgagcag ctgggcttct 540
ttgacaactt catcgatttt aatacctttg ccgccatctt ttactgacca tcgctcaacg 600
ttgcaccttc cagcgctggc gtgatcattt cagcgctggc cgacgaanaa gtgctggtat 660
cgagcgtcac ttctactttc cagtgggttg ccgttacgca caagc 705

```

```

<210> 260
<211> 216
<212> PRT
<213> Mus musculus

```

```

<220>
<221> MOD_RES
<222> (19)
<223> XAA = ANYTHING

```

```
<400> 260
```

```

Leu Cys Val Thr Ala Asn His Trp Lys Val Glu Val Thr Leu Asp Thr
  1             5             10             15

```

```

Ser Thr Xaa Ser Ser Ala Ser Ala Glu Met Ile Thr Pro Ala Leu Glu
      20             25             30

```

```

Gly Ala Thr Leu Ser Asp Gly Gln Lys Met Ala Ala Lys Val Leu Lys
  35             40             45

```

```

Ser Met Lys Leu Ser Lys Lys Pro Ser Cys Ser Gly Trp Leu Ala Lys
  50             55             60

```

```

Arg Arg Cys Asp His Trp Arg Gln Pro Arg Ser Gly Glu Leu Asp Cys
  65             70             75             80

```

```

Asn Ala Ser Ala Gly Gly Lys Thr Gly His His Arg Pro Ala Asn Cys
      85             90             95

```

```

Thr Arg Gln Lys His Leu Ser Ala Asp Ala Leu Met Ser Thr Gly His
  100            105            110

```

```

Gln Ala Tyr Val Cys Pro Val Asn Ser Trp Tyr Ala Ala Ala Val Pro
  115            120            125

```

```

Phe Phe Asn Asp Ala Ser Ile Met Phe Val Lys Leu Leu Arg Ser Val
  130            135            140

```

```

Ala Ile Gly Leu Ile Val Gly Ala Ile Leu Leu Val Ala Met Pro Ser
  145            150            155            160

```

```

Leu Arg Ser Leu Asn Pro Leu Ser Thr Pro Gln Phe Asp Ser Thr Asp

```

165

170

175

Glu Thr Pro Ala Ser Tyr Asn Leu Ala Val Arg Arg Ala Ala Pro Ala
 180 185 190

Val Val Asn Val Tyr Asn Arg Gly Leu Asn Thr Asn Ser His Asn Gln
 195 200 205

Leu Glu Ile Arg Thr Leu Gly Ser
 210 215

<210> 261

<211> 685

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (1)..(295)

<223> N = A, C, G OR T/U

<400> 261

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ncattcctga aggaccccccac ncgatgcttt ttaantaaca agtntgcagc cattgntgnt 60
ctgcgcgagg agtccacacc tcagtcgcct ctgccacgtc tgttgccaca aagaagacag 120
agcaaggccc accatcctcc gagtacattt ttgaacggga atctaaatat ggtgcacaca 180
attaccatcc tttgcctgta gccctggaga gaggaaaagg catttatatg tgggatgtgg 240
aaggcaggca gtacttcgat ttcctgagtg cttatggtgc tgtcagccaa ggacnctgcc 300
acccaaagat catagatgcc atgaagagtc aggtggacaa gctgacatta acatctcggg 360
ctttctataa caatgtcctt ggtgaatacg aggagtacat caccaagctt ttcaactaca 420
acaaagttct ccctatgaat acaggagtgg aggctggaga gactgcatgt aagctcgtctc 480
gtcgttgggg ctacaccgtg aaaggcatcc agaaatacaa agcaaagatt gtttttgctg 540
atgggaactt ttgggggtcga acactatctg caatctccag ttccacagat ccgaccagtt 600
atgatggctt tggacccttc atgccaggct ttgaaaccat cccatataac gatctgcccg 660
cactggagcg tgctcttcag gatcc 685

```

<210> 262

<211> 217

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (6)..(18)

<223> XAA = ANYTHING

<400> 262

His Ser Arg Thr Pro Xaa Asp Ala Phe Xaa Thr Ser Xaa Gln Pro Leu
 1 5 10 15

Xaa Xaa Cys Ala Arg Ser Pro His Leu Ser Arg Leu Cys His Val Cys
 20 25 30

Cys His Lys Glu Asp Arg Ala Arg Pro Thr Ile Leu Arg Val His Phe

35

40

45

Thr Gly Ile Ile Trp Cys Thr Gln Leu Pro Ser Phe Ala Cys Ser Pro
 50 55 60

Gly Glu Arg Lys Arg His Leu Tyr Val Gly Cys Gly Arg Gln Ala Val
 65 70 75 80

Leu Arg Phe Pro Glu Cys Leu Trp Cys Cys Gln Pro Arg Thr Leu Pro
 85 90 95

Pro Lys Asp His Arg Cys His Glu Glu Ser Gly Gly Gln Ala Asp Ile
 100 105 110

Asn Ile Ser Gly Phe Leu Gln Cys Pro Trp Ile Arg Gly Val His His
 115 120 125

Gln Ala Phe Gln Leu Gln Gln Ser Ser Pro Tyr Glu Tyr Arg Ser Gly
 130 135 140

Gly Trp Arg Asp Cys Met Ala Arg Ser Ser Leu Gly Leu His Arg Glu
 145 150 155 160

Arg His Pro Glu Ile Gln Ser Lys Asp Cys Phe Cys Trp Glu Leu Leu
 165 170 175

Gly Ser Asn Thr Ile Cys Asn Leu Gln Phe His Arg Ser Asp Gln Leu
 180 185 190

Trp Leu Trp Thr Leu His Ala Arg Leu Asn His Pro Ile Arg Ser Ala
 195 200 205

Arg Thr Gly Ala Cys Ser Ser Gly Ser
 210 215

<210> 263

<211> 702

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (651)..(699)

<223> N = A, C, G OR T/U

<400> 263

cttagcatct tttactttca ccagcgtttc tgggtgggat ccaggggaatc ctgcagttcc 60
 aggagggcca gggggaccag gttgcccatc actgccccga gcaccatcat tgccctcgagc 120
 acctgcagct ccaggaaggc ctggtcgctc tcgctcacca ggagcccctc taggacctat 180
 gggggccagga gctccgttgt ctccctggaag accattttca ccttcagtc caggagcacc 240
 tgtttctccc ttttctccat tgcgtccatc aaagcctctg tgcctttca taccagggaa 300
 tccaggcattg ccagctgggc ctttgatacc tggaggtcca ggcagtcac gctctccagg 360
 tcgtccaggt cttctgact ctccatcctt tccagcagga ccagctggac caagagcacc 420
 aggaggtcct ggagggcctg ctggaccagc ttgaccaggt tcaccagggg gaccttggtta 480

```
tccaggagaa ccaggagatc caggatgtcc agaagaacca gggggtcctg gagggcctgg 540
tggaccagct ggtcccggat agccacccat tcttccactt cagacttgac atcatatgag 600
tcgaattggg gagaataatt ttggccacca gttggacatg attacagatt ncangggagc 660
caggaagccc anggagacct gggtgtcctg gaanggcang gt 702
```

<210> 264

<211> 220

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (2)..(18)

<223> XAA = ANYTHING

<400> 264

```
Thr Xaa Pro Phe Gln Asp Asn Gln Val Ser Xaa Gly Phe Leu Ala Pro
  1              5              10              15

Xaa Xaa Ser Val Ile Met Ser Asn Trp Trp Pro Lys Leu Phe Ser Pro
      20              25              30

Ile Arg Leu Ile Cys Gln Val Ser Gly Arg Met Gly Gly Tyr Pro Gly
      35              40              45

Pro Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Ser Gly His
      50              55              60

Pro Gly Ser Pro Gly Ser Pro Gly Tyr Gln Gly Pro Pro Gly Glu Pro
      65              70              75              80

Gly Gln Ala Gly Pro Ala Gly Pro Pro Gly Pro Pro Gly Ala Leu Gly
      85              90              95

Pro Ala Gly Pro Ala Gly Lys Asp Gly Glu Ser Gly Arg Pro Gly Arg
      100              105              110

Pro Gly Glu Arg Gly Leu Pro Gly Pro Pro Gly Ile Lys Gly Pro Ala
      115              120              125

Gly Met Pro Gly Phe Pro Gly Met Lys Gly His Arg Gly Phe Asp Gly
      130              135              140

Arg Asn Gly Glu Lys Gly Glu Thr Gly Ala Pro Gly Leu Lys Gly Glu
      145              150              155              160

Asn Gly Leu Pro Gly Asp Asn Gly Ala Pro Gly Pro Met Gly Pro Arg
      165              170              175

Gly Ala Pro Gly Glu Arg Gly Arg Pro Gly Leu Pro Gly Ala Ala Gly
      180              185              190

Ala Arg Gly Asn Asp Gly Ala Arg Gly Ser Asp Gly Gln Pro Gly Pro
      195              200              205
```

Pro Gly Pro Pro Gly Thr Ala Gly Phe Pro Gly Ser
 210 215 220

<210> 265
 <211> 691
 <212> DNA
 <213> Mus musculus
 <220>
 <221> modified_base
 <222> (19)..(187)
 <223> N = A, C, G OR T/U

<400> 265
 tttctttgtt gctttaacnt atcaaggggt ttttgetctg cattcatgag tgcngttggg 60
 tagtttttcc attgctcaca aagctttgtg tgtacaagga cttcaagaag cacggtgcc 120
 aagaaagatt tgttgctctg accttttggg gatgtttatc ccatatcttt acgggctcta 180
 cctcatntgg gctgtgtttg agatgttcac tcctatcctg gaaagaagcg ggtcggagat 240
 cccccccgac gttgtgctgg cctccatcct ggctgtctgt gtgatgatcc tctcttccta 300
 ttttattacc ttcatctacc ttgtgaacag cacaaagaaa accattctga ctctaatact 360
 ggtgtgcgcg gtcaccttcc tccttgtctg cagtggagcc tttttcccat atagttctaa 420
 tcccagagat ccaaagccaa agagagtgtt tcttcagcac gtgagtagaa cttttcataa 480
 cttagaagga agcgtagtaa aaagagactc tggaatatgg atcaatgggt ttgattatac 540
 tggaatgtct cacgtaacac ctcacattcc tgagatcaac gacacaatcc gagctcactg 600
 tgaggaggat gcccactct gtggcttccc ttggtatctt ccagtgcact tcctgatcag 660
 gaaaaactgg tatcttccaa cccccggatc c 691

<210> 266
 <211> 229
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (17)..(61)
 <223> XAA = ANYTHING

<400> 266
 Phe Phe Val Ala Leu Thr Tyr Gln Gly Val Phe Ala Leu His Ser Val
 1 5 10 15
 Xaa Leu Gly Ser Phe Ser Ile Ala His Lys Ala Leu Cys Val Gln Gly
 20 25 30
 Leu Gln Glu Ala Arg Cys Pro Arg Lys Ile Cys Cys Ser Asp Leu Leu
 35 40 45
 Gly Met Phe Ile Pro Tyr Leu Tyr Gly Leu Tyr Leu Xaa Trp Ala Val
 50 55 60
 Phe Glu Met Phe Thr Pro Ile Leu Glu Arg Ser Gly Ser Glu Ile Pro
 65 70 75 80

Pro Asp Val Val Leu Ala Ser Ile Leu Ala Val Cys Val Met Ile Leu
85 90 95

Ser Ser Tyr Phe Ile Thr Phe Ile Tyr Leu Val Asn Ser Thr Lys Lys
100 105 110

Thr Ile Leu Thr Leu Ile Leu Val Cys Ala Val Thr Phe Leu Leu Val
115 120 125

Cys Ser Gly Ala Phe Phe Pro Tyr Ser Ser Asn Pro Glu Ser Pro Lys
130 135 140

Pro Lys Arg Val Phe Leu Gln His Val Ser Arg Thr Phe His Asn Leu
145 150 155 160

Glu Gly Ser Val Val Lys Arg Asp Ser Gly Ile Trp Ile Asn Gly Phe
165 170 175

Asp Tyr Thr Gly Met Ser His Val Thr Pro His Ile Pro Glu Ile Asn
180 185 190

Asp Thr Ile Arg Ala His Cys Glu Glu Asp Ala Pro Leu Cys Gly Phe
195 200 205

Pro Trp Tyr Leu Pro Val His Phe Leu Ile Arg Lys Asn Trp Tyr Leu
210 215 220

Pro Thr Pro Gly Ser
225

<210> 267

<211> 671

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (6)

<223> N = A, C, G OR T/U

<400> 267

tgtttnacat attgttaaca tttttaaaaa gtgtgtgctt gtatgtatgt tgagggcatg 60
atatgtgcac aagagggcagg gcctgaaaag ggaggccagg agaaagtgtc agatacttac 120
aggggggtcac aagcctcctg ttgtagggaa tcagccttgg atcttttgca agaaccatac 180
ttgaatttaa ctggagacat ctttccagtc cctagaaatt taatttgtat ttgagtgaag 240
gttgtcaaga ttttctgtta cctatgttaa actgagtctt tgtttgtttg tttcgcacgc 300
cctcttttctt ttttaagttag cgcacagagc ggtgtgtttt gtgatgacat ttgcttgtgt 360
agttattgct gtgctttttt cttaaacatc ctttcccag ctgacttttt ttttcccctt 420
gctttttaat tttatatgga tttgtgtcat gatatcatgg aacgttggtg aaacactgga 480
atctagcctt ttgttttcta gattgagaac gtgaaatcca tgctaaatat ctactgacat 540
gtccacatct tgatgttggg gcagagctga gactcaaagt catcttattc aagtgtcatg 600
tgttctttat gataccatat tattaccttg tgcaatatgt aattttcatt ttgtgttttc 660
cccctggatc c 671

<210> 268
 <211> 211
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (2)
 <223> XAA = ANYTHING

<400> 268
 Phe Xaa Ile Leu Leu Thr Phe Leu Lys Ser Val Cys Leu Tyr Val Cys
 1 5 10 15
 Gly His Asp Met Cys Thr Arg Gly Arg Ala Lys Gly Arg Pro Gly Glu
 20 25 30
 Ser Val Arg Tyr Leu Gln Gly Val Thr Ser Leu Leu Leu Gly Ile Ser
 35 40 45
 Leu Gly Ser Phe Ala Arg Thr Ile Leu Glu Phe Asn Trp Arg His Leu
 50 55 60
 Ser Ser Pro Lys Phe Asn Cys Asp Leu Ser Glu Gly Cys Gln Asp Phe
 65 70 75 80
 Leu Leu Pro Met Leu Asn Val Phe Val Cys Leu Phe Arg Thr Pro Ser
 85 90 95
 Phe Phe Leu Ser Arg Thr Glu Arg Cys Val Leu His Leu Leu Val Leu
 100 105 110
 Leu Leu Cys Phe Phe Leu Lys His Pro Phe Pro Ser Leu Phe Phe Ser
 115 120 125
 Pro Cys Phe Leu Ile Leu Tyr Gly Phe Val Ser Tyr His Gly Thr Leu
 130 135 140
 Leu Lys His Trp Asn Leu Ala Phe Cys Phe Leu Asp Glu Arg Glu Ile
 145 150 155 160
 His Ala Lys Tyr Leu Leu Thr Cys Pro His Leu Asp Val Gly Ala Glu
 165 170 175
 Leu Arg Leu Lys Val Ile Leu Phe Lys Cys His Val Phe Phe Met Ile
 180 185 190
 Pro Tyr Tyr Tyr Leu Val Gln Tyr Val Ile Phe Ile Leu Cys Phe Pro
 195 200 205
 Pro Gly Ser
 210

<210> 269
 <211> 684
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (125)..(153)
 <223> N = A, C, G OR T/U

<400> 269
 acctcagtga tgtgcaagggt tgatcaatga tccgtgagtc tctctcatct cagtgtgtgg 60
 agtgcaagag tagagaactc agatgccaac taattcttga gcatggataa ccaaatttca 120
 ggggnaggagc cgtttttcaat agctaaaagt gcntgagtta taatcacctt gtcacgtttt 180
 gggtgggttc tgaatttgca taccaaccag agcatgaaca ccagtccaca gcatatggca 240
 gcaccaaaca aaatcactcc caccatttcc tttaaagtaag aaaaagcaga ggtaagccaa 300
 gaggtaaagt ctccgagggt cactgggttcc actctgggtcc cattaaggct caggatctgc 360
 atctgcagtc tctgttgcaa cctttccagc tcctgcgacc agttcccctt caggtaactc 420
 gataggtctg tacttttaat aaaagaatta ttaatatacc tattgggagt aatgcacaca 480
 tgcaaagtgg atgccacaca actcatttgt atgacatcca tcatctgttc catgtcatgt 540
 tgtaaaatat ccactctgat tactaacaat taaccctgag gtgatatgag aatccaccct 600
 ttgcagggtgta agcaatgcct cagacgtttt ttctgctatc tgacttatag tgtcagcagt 660
 attaatttga tctgccctgg atcc 684

<210> 270
 <211> 220
 <212> PRT
 <213> Mus musculus

 <220>
 <221> MOD_RES
 <222> (40)
 <223> XAA = ANYTHING

<400> 270
 Thr Ser Val Met Cys Lys Gly Asp Gln Ser Val Ser Leu Ser His Leu
 1 5 10 15
 Ser Val Trp Ser Ala Arg Val Glu Asn Ser Asp Ala Asn Phe Leu Ser
 20 25 30
 Met Asp Asn Gln Ile Ser Gly Xaa Glu Pro Phe Ser Ile Ala Lys Ser
 35 40 45
 Ala Val Ile Ile Thr Leu Ser Arg Phe Gly Trp Val Leu Asn Leu His
 50 55 60
 Thr Asn Gln Ser Met Asn Thr Ser Pro Gln His Met Ala Ala Pro Asn
 65 70 75 80
 Lys Ile Thr Pro Thr His Ser Leu Lys Glu Lys Ala Glu Val Ser Gln
 85 90 95

Glu Val Lys Ser Pro Arg Val Thr Gly Ser Thr Leu Val Pro Leu Arg
 100 105 110
 Leu Arg Ile Cys Ile Cys Ser Leu Val Cys Asn Leu Ser Ser Ser Cys
 115 120 125
 Asp Gln Phe Pro Phe Arg Leu Asp Arg Ser Val Leu Leu Ile Lys Glu
 130 135 140
 Leu Leu Ile Tyr Leu Leu Gly Val Met His Thr Cys Lys Val Asp Ala
 145 150 155 160
 Thr Gln Leu Ile Cys Met Thr Ser Ile Ile Cys Ser Met Ser Cys Cys
 165 170 175
 Lys Ile Ser Thr Leu Ile His His Pro Gly Asp Met Arg Ile His Pro
 180 185 190
 Leu Gln Gly Lys Gln Cys Leu Arg Arg Phe Phe Cys Tyr Leu Thr Tyr
 195 200 205
 Ser Val Ser Ser Ile Asn Leu Ile Cys Pro Gly Ser
 210 215 220

<210> 271

<211> 703

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (610)..(695)

<223> N = A, C, G OR T/U

<400> 271

cttcagcatc ttttactttc accagcgttt ctgggtggga tcttgagcag gggctccagg 60
 ggccccagga tgcccaggcc ccatgtgtgg ggcaggtctt ctgggtgtca caggcctgtg 120
 attgctgggc ctctcctggg cagtggcccc cacacttagg agcaggatta tcacatactc 180
 gttgacggat ctgggttcct ttggagcatg tgacagagca aggccccag ggtccccact 240
 cagaccagcc acccatctct ggacagcatg gctggtcctc acaggcctgt agctgccact 300
 caagagttcc aggagccaca ttctcagagc actgaccacc tctgcccaca cagcgctgt 360
 gtcgcagctg ggacccctca gaacatgtaa ctgagcaggg ccccccataag gaccatgctg 420
 accattgtgg agacctgcat gcctgacaga ggccaccatc atgctcctgg aaggcatagg 480
 cagcgttgag acagcagtct tctaccctga tgtctctccc aagtaggcct ttgcacctgc 540
 cagaggactc ctcatactgg gtgaagcaaa gcacagggtc tgagcctgtg gctggcagga 600
 taaccagtan cagcaggagc cactgagggg cttgcatttc ancangcatt ttgaacacta 660
 tgtttctgca ctctacaaa aaagangcgt cnacnccggc cgc 703

<210> 272

<211> 221

<212> PRT

<213> Mus musculus

Category	Mean	SD	Median	Mode	Range	Skewness	Kurtosis
Age	35.5	10.5	35	35	25-55	-0.1	2.5
Gender	1.5	0.5	1	1	1-2	0.1	3.5
Marital Status	2.5	1.0	2	2	1-4	-0.2	2.0
Education	12.5	2.0	12	12	10-16	-0.1	2.5
Occupation	1.5	0.5	1	1	1-2	0.1	3.5
Religion	1.5	0.5	1	1	1-2	0.1	3.5
Political Party	1.5	0.5	1	1	1-2	0.1	3.5
Income	15.5	5.0	15	15	10-25	-0.1	2.5
Health	1.5	0.5	1	1	1-2	0.1	3.5
Stress	2.5	1.0	2	2	1-4	-0.2	2.0
Life Satisfaction	3.5	1.0	3	3	1-5	-0.1	2.5
Work Satisfaction	2.5	1.0	2	2	1-4	-0.2	2.0
Family Satisfaction	3.5	1.0	3	3	1-5	-0.1	2.5
Community Satisfaction	2.5	1.0	2	2	1-4	-0.2	2.0
Overall Satisfaction	2.5	1.0	2	2	1-4	-0.2	2.0

Ala Ala Gly Val Asp Ala Ser Phe Leu Glu Cys Arg Asn Ile Val Phe
1 5 10 15

Val Ile Leu Pro Ala Thr Gly Ser Asp Pro Val Leu Cys Phe Thr Gln
35 40 45

Arg Val Glu Asp Cys Cys Leu Asn Ala Ala Tyr Ala Phe Gln Glu His
65 70 75 80

Ser Leu Trp Gly Pro Cys Ser Val Thr Cys Ser Glu Gly Ser Gln Leu
100 105 110

Ala Pro Gly Thr Leu Glu Trp Gln Leu Gln Ala Cys Glu Asp Gln Pro
130 135 140

Cys Ser Val Thr Cys Ser Lys Gly Thr Gln Ile Arg Gln Arg Val Cys
165 170 175

Gln Ser Gln Ala Cys Asp Thr Gln Lys Thr Cys Pro Thr His Gly Ala
195 200 205

<210> 273
<211> 685
<212> DNA
<213> Mus musculus

160

<221> modified_base
 <222> (10)..(78)
 <223> N = A, C, G OR T/U

<400> 273

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aaaaaaagtn aagttggcct tgtgcgtaac ggccaaccca ctgaaagtag aagtgacggt 60
tcgataccag cacttnttng tcggccagcg ttgaaatgat cacgccagcg tggaaggtgc 120
aacgttgagc gatggtcagc taaaagatgg cggcaaaggt attaaaatcg atgaagttgt 180
caaagaagcc cagctgctca ggctggcttg caaaaagacg atgtgatcat tggcgtcaac 240
cgcgatcggg tgaactcgat tgctgaaatg cgtaaagtgc tgcggcaaaa ccggccatca 300
tcgccctgca aattgtacgc ggcaatgaaa gcatctatct gctgatgcgt taatgtcgta 360
aacggggcat caggcttacg tgtgatgtcc ggtaaactcg tggatgctg ctgccgttcc 420
cttttttaat gacgcctcca tcatgtttgt gaagctctta cgttccgttg cgattggatt 480
aattgtcggc gctattctgc tggttgccat gccttcgctg cgcagcctta acccgctttc 540
cactccgcaa tttgacagta ccgatgagac gcctgccagc tataatctgg cggttcgccg 600
cgccgcgcca gcggtgggta acgtttacaa ccgtgggttg aacaccaact ctcacaacca 660
gcttgagatc cgcaccctgg gatcc                                     685

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<210> 274

<211> 222

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (25)

<223> XAA = ANYTHING

<400> 274

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Lys Lys Val Lys Leu Ala Leu Cys Val Thr Ala Asn Pro Leu Lys Val
 1              5              10              15

Glu Val Thr Val Arg Tyr Gln His Xaa Xaa Val Gly Gln Arg Asn Asp
      20              25              30

His Ala Ser Val Glu Gly Ala Thr Leu Ser Asp Gly Gln Leu Lys Asp
      35              40              45

Gly Gly Lys Gly Ile Lys Ile Asp Glu Val Val Lys Glu Ala Gln Leu
      50              55              60

Leu Arg Leu Ala Cys Lys Lys Thr Met Ser Leu Ala Ser Thr Ala Ile
      65              70              75              80

Gly Thr Arg Leu Leu Lys Cys Val Lys Cys Cys Gly Lys Thr Gly His
      85              90              95

His Arg Pro Ala Asn Cys Thr Arg Gln Lys His Leu Ser Ala Asp Ala
      100             105             110

Leu Met Ser Thr Gly His Gln Ala Tyr Val Cys Pro Val Asn Ser Trp
      115             120             125

Tyr Ala Ala Ala Val Pro Phe Phe Asn Asp Ala Ser Ile Met Phe Val

```

130	135	140
Lys Leu Leu Arg Ser Val Ala Ile Gly Leu Ile Val Gly Ala Ile Leu		
145	150	155 160
Leu Val Ala Met Pro Ser Leu Arg Ser Leu Asn Pro Leu Ser Thr Pro		
	165	170 175
Gln Phe Asp Ser Thr Asp Glu Thr Pro Ala Ser Tyr Asn Leu Ala Val		
	180	185 190
Arg Arg Ala Ala Pro Ala Val Val Asn Val Tyr Asn Arg Gly Leu Asn		
	195	200 205
Thr Asn Ser His Asn Gln Leu Glu Ile Arg Thr Leu Gly Ser		
	210	215 220

<210> 275
 <211> 703
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (656)..(698)
 <223> N = A, C, G OR T/U

<400> 275
 cttcagcatc ttttactttc accagcgttt ctgggtggga tccctgttcc tgactgtctg 60
 agatgaggct tagccaactc tgttcctgag tgaatctgcc cagcagatag ttaatagtaa 120
 tccaccata ggcaccttcc tcttgctcag tgatgatctt ggcaccctgg aagtcaaagg 180
 ggtagctctt aaggcttggt gacactgcag ccaggacctc gtctgccgat tgttcgcttt 240
 ccattctaag caagcgcgat cctgctgtgg ctcccaggta gacaggagtc tggatgatgct 300
 tggatgttgg tatcagttcg gtggacagtt ccatgcattc ggccaggtag gcaccgattt 360
 catctgtttt ctgagcatat tttgagattc caggaccttt cacttggcat tcctctaact 420
 gctgcaccac cctgtgtgca ttctccttct cgcccgccca cttgtagatg tacaggtttg 480
 tgtgagatga ccccgcatcc aacacaatcc catacttaac attttctggc aaaggtttgt 540
 tctgggtcag tcccacagca atcaaagcta tcacagccaa gatagagggtg aaaccaagga 600
 tgatcaagaa tatttttgga gcaaaatctc ttcaccttag aatcctttat atcttncata 660
 aggggcaagc tttttggttc ctttctcttc ctcgctgnct tgg 703

<210> 276
 <211> 220
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (2)..(7)
 <223> XAA = ANYTHING

<400> 276
 Pro Xaa Gln Arg Gly Arg Xaa Arg Asn Gln Lys Ala Cys Pro Leu Xaa

1	5	10	15
Lys Ile Arg Ile Leu Arg Arg Asp Phe Ala Pro Lys Ile Phe Leu Ile			
20	25	30	
Ile Leu Gly Phe Thr Ser Ile Leu Ala Val Ile Ala Leu Ile Ala Val			
35	40	45	
Gly Leu Thr Gln Asn Lys Pro Leu Pro Glu Asn Val Lys Tyr Gly Ile			
50	55	60	
Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu Tyr Ile Tyr Lys Trp			
65	70	75	80
Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val Gln Gln Leu Glu Glu			
85	90	95	
Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr Ala Gln Lys Thr Asp			
100	105	110	
Glu Ile Gly Ala Tyr Leu Ala Glu Cys Met Glu Leu Ser Thr Glu Leu			
115	120	125	
Ile Pro Thr Ser Lys His His Gln Thr Pro Val Tyr Leu Gly Ala Thr			
130	135	140	
Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Gln Ser Ala Asp Glu			
145	150	155	160
Val Leu Ala Ala Val Ser Thr Ser Leu Lys Ser Tyr Pro Phe Asp Phe			
165	170	175	
Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp			
180	185	190	
Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr Gln Glu Gln Ser Trp			
195	200	205	
Leu Ser Leu Ile Ser Asp Ser Gln Glu Gln Gly Ser			
210	215	220	

<210> 277

<211> 719

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (628)..(666)

<223> N = A, C, G OR T/U

<400> 277

cttcagcatc ttttctttca ccagcgtttc tgggtgggat ccaggggtgg ggtggaaaac 60
 ttgctaataaa caaagcaa atgtctttcaat attcacaacc ttaaaattat atccaagaaa 120

```

acaaaggata aataattttt tataaaaata attacttctc aaataacggt tcacaataga 180
cctgctcaat acatcgatct gactcatctc atctgtgccg cttttcttct ttttaaaatt 240
ctggcctggg acaaaactac atgaaagaaa gtaccattaa attaagggtt actttccaaa 300
aaacaataga aaaatcttaa aagtaaattc acttatatat aaaatattaa ggcctctgca 360
tgagaacggt ttaacatctg gggaactggc ctttcctaac tgacctatga cccactcac 420
ctcaaacttc agaataaaag gttctggagt gaaaagtcc ttttaatttg ccaatacatg 480
aaattacaca taaaattaca ctgcaaagta atatgtactt aacaaatgat atattgaaaa 540
gtctaacttt ctgctggcta atttcagtat ggacttcaga tcaagtatag tgtattttca 600
gccatatctc ataatctttt gcgacgcngn cgcgattca agcttactct tnccttttca 660
attcanaaga actcgtcaag aaggcgatag aaggcgatgc gctgcgaatc gggagccgg 719

```

<210> 278

<211> 219

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (17) .. (28)

<223> XAA = ANYTHING

<400> 278

```

Gly Ser Arg Phe Ala Ala His Arg Leu Leu Ser Pro Ser Arg Val Leu
  1              5              10              15

```

```

Xaa Asn Lys Xaa Lys Ser Lys Leu Glu Phe Ala Xaa Ala Ser Gln Lys
      20              25              30

```

```

Ile Met Arg Tyr Gly Lys Tyr Thr Ile Leu Asp Leu Lys Ser Ile Leu
      35              40              45

```

```

Lys Leu Ala Ser Arg Lys Leu Asp Phe Ser Ile Tyr His Leu Leu Ser
      50              55              60

```

```

Thr Tyr Tyr Phe Ala Val Phe Tyr Val Phe His Val Leu Ala Lys Leu
      65              70              75              80

```

```

Lys Gly Leu Phe Thr Pro Glu Pro Phe Ile Leu Lys Phe Glu Val Ser
      85              90              95

```

```

Gly Val Ile Gly Gln Leu Gly Lys Ala Ser Ser Pro Asp Val Lys Pro
      100              105              110

```

```

Phe Ser Cys Arg Gly Leu Asn Ile Leu Tyr Ile Ser Glu Phe Thr Phe
      115              120              125

```

```

Lys Ile Phe Leu Leu Phe Phe Gly Lys Pro Leu Ile Trp Tyr Phe Leu
      130              135              140

```

```

Ser Cys Ser Phe Val Pro Gly Gln Asn Phe Lys Lys Lys Lys Ser Gly
      145              150              155              160

```

```

Thr Asp Glu Met Ser Gln Ile Asp Val Leu Ser Arg Ser Ile Val Lys
      165              170              175

```


Arg Tyr Leu Arg Ser Asn Tyr Phe Tyr Lys Lys Leu Phe Ile Leu Cys
 180 185 190

Phe Leu Gly Tyr Asn Phe Lys Val Val Asn Ile Glu Arg His Leu Leu
 195 200 205

Cys Phe Gln Val Phe His Pro Thr Pro Gly Ser
 210 215

<210> 279
 <211> 703
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (582)..(701)
 <223> N = A, C, G OR T/U

<400> 279
 cttcgcacatct tttacttttcc cagcggtttct ggggtgggac cagcagcaag ttccaccatg 60
 atgctctcac cattctttgt gatgaaaggt gtgatgaaga caaagaacac atcgtagatg 120
 agaagaaggc ctagcagtat cacgcatgac atgaaattgg gtaacttcat tgttttaatt 180
 aagttgagac agaaagcaat tctaagata tcctgtaaaa tccaagccca cctatcctca 240
 tttcgaaata cagcccacac aacagcaact gagatgcaca gcccggaag gaaaatcagg 300
 ctcaatttaa tgtttttgcc acaacacaaa atcgtgcact gtccacatgg catcctatga 360
 atcaatgcag aaagacagtt gtacaggctc attgacgatg ctatgcagaa aatcgctatc 420
 ataacataca caagccacct gtagaagaaa tacagtaaga caatgtcgac gcggccgcga 480
 attcaagctt actcttccctt tttcaattca gaagaactcg tcaagaaggc gatagaaggc 540
 gatgcgctgc gaatcgggag cggcgatacc gttaaagcac angaagcggg caggccattc 600
 gccgncaagc tcttcacaat atcacgggta gncaacgcta tgtcctgata gcggtccgnc 660
 acaccagcc cggncacagt cgatgaatnc agaaaagcgg nct 703

<210> 280
 <211> 220
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (1)..(33)
 <223> XAA = ANYTHING

<400> 280
 Xaa Ala Phe Leu Xaa Ser Ser Thr Val Xaa Gly Leu Gly Val Xaa Asp
 1 5 10 15

Arg Tyr Gln Asp Ile Ala Leu Xaa Thr Arg Asp Ile Val Lys Ser Leu
 20 25 30

Xaa Ala Asn Gly Leu Thr Ala Ser Ser Cys Phe Thr Val Ser Pro Leu
 35 40 45

Pro Ile Arg Ser Ala Ser Pro Ser Ile Ala Phe Leu Thr Ser Ser Ser
 50 55 60
 Glu Leu Lys Lys Glu Glu Ala Ile Arg Gly Arg Val Asp Ile Val Leu
 65 70 75 80
 Leu Tyr Phe Phe Tyr Arg Trp Leu Val Tyr Val Met Ile Ala Ile Phe
 85 90 95
 Cys Ile Ala Ser Ser Met Ser Leu Tyr Asn Cys Leu Ser Ala Leu Ile
 100 105 110
 His Arg Met Pro Cys Gly Gln Cys Thr Ile Leu Cys Cys Gly Lys Asn
 115 120 125
 Ile Lys Val Ser Leu Ile Phe Leu Ser Gly Leu Cys Ile Ser Val Ala
 130 135 140
 Val Val Trp Ala Val Phe Arg Asn Glu Asp Arg Trp Ala Trp Ile Leu
 145 150 155 160
 Gln Asp Ile Leu Gly Ile Ala Phe Cys Leu Asn Leu Ile Lys Thr Met
 165 170 175
 Lys Leu Pro Asn Phe Met Ser Cys Val Ile Leu Leu Gly Leu Leu Leu
 180 185 190
 Ile Tyr Asp Val Phe Phe Val Phe Ile Thr Pro Phe Ile Thr Lys Asn
 195 200 205
 Gly Glu Ser Ile Met Val Glu Leu Ala Ala Gly Ser
 210 215 220

<210> 281

<211> 722

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (698)

<223> N = A, C, G OR T/U

<400> 281

cttcagcatc ttttactttc accagcggtt ctgggtggga tcctgtcgat gtgacccat 60
 gactaggtaa gtgtggttca actttaacgt aaatatcatt cttccagaca tatgccaact 120
 tatgaccttc tggtgacct gtgatccact gtgtattatt tggaatcttc tcttctgtga 180
 tcagctgtct tttattcaca tcataaatgt tgtatgaagc tgtgtaggaa tgtctccatt 240
 gcttcacgta gttgtattcc aagagaacaa acagtcgggc aggtgacact gaatgatatc 300
 caaagctttc aaaggtactg ttctccaaga aaatggagct gtttccatgt tcagcattga 360
 gcagcaagat attgttctct tgtttgtaga ggtattcaaa gtctgaaacc caccacaaag 420
 agtaggactt gacctgaaag gtactcttta aatagtcagc tagtgaatac gttctgcggc 480
 tgtcagctgc cgcttcactt ttgctcagca gaactattgg cacgggtgatg atgggtgacaa 540

```

gcgcgagcgac accaagcagt cccagaagaa ccttccacgg tgtcttcatg gtcgggcggc 600
tccttgaaac tgaactctga agcttgagcg cagcagaagt cactgcgcgc agagacggac 660
gtccgctcgac gccggccgcg aattcaagct tactcttnc ttttcaattc agaagaactc 720
gt
722

```

```

<210> 282
<211> 227
<212> PRT
<213> Mus musculus
.
<220>
<221> MOD_RES
<222> (7)
<223> XAA = ANYTHING

```

```

<400> 282
Arg Val Leu Leu Asn Lys Xaa Lys Ser Lys Leu Glu Phe Ala Ala Gly
  1             5             10             15
Val Asp Gly Arg Pro Ser Leu Arg Ala Val Thr Ser Ala Ala Leu Lys
      20             25             30
Leu Gln Ser Ser Val Ser Arg Ser Arg Pro Thr Met Lys Thr Pro Trp
      35             40             45
Lys Val Leu Leu Gly Leu Leu Gly Val Ala Ala Leu Val Thr Ile Ile
      50             55             60
Thr Val Pro Ile Val Leu Leu Ser Lys Asp Glu Ala Ala Ala Asp Ser
      65             70             75             80
Arg Arg Thr Tyr Ser Leu Ala Asp Tyr Leu Lys Ser Thr Phe Arg Val
      85             90             95
Lys Ser Tyr Ser Leu Trp Trp Val Ser Asp Phe Glu Tyr Leu Tyr Lys
      100            105            110
Gln Glu Asn Asn Ile Leu Leu Leu Asn Ala Glu His Gly Asn Ser Ser
      115            120            125
Ile Phe Leu Glu Asn Ser Thr Phe Glu Ser Phe Gly Tyr His Ser Val
      130            135            140
Ser Pro Asp Arg Leu Phe Val Leu Leu Glu Tyr Asn Tyr Val Lys Gln
      145            150            155            160
Trp Arg His Ser Tyr Thr Ala Ser Tyr Asn Ile Tyr Asp Val Asn Lys
      165            170            175
Arg Gln Leu Ile Thr Glu Glu Lys Ile Pro Asn Asn Thr Gln Trp Ile
      180            185            190
Thr Trp Ser Pro Glu Gly His Lys Leu Ala Tyr Val Trp Lys Asn Asp
      195            200            205

```

Ile Tyr Val Lys Val Glu Pro His Leu Pro Ser His Arg Ile Thr Ser
 210 215 220

Thr Gly Ser
 225

<210> 283
 <211> 701
 <212> DNA
 <213> Mus musculus
 <220>
 <221> modified_base
 <222> (558)..(701)
 <223> N = A, C, G OR T/U

<400> 283
 cttcagcatc ttttactttc accagcgttt ctgggtggga tccgttttctt ttctctaaat 60
 ctttaattct gaactggcct tgagcgggct tgcttttctt gtcttttatag taggcaatga 120
 gttgaactgt gtagttctgc tctggcagaa ggccttgaat aatcgctttt gttgcagtgt 180
 tctggagatt catctgggtg gtcttttctc ctgaagctgg agccacgagc agtttgtagc 240
 caccaaaattt cctctcttggg gcttttccatg aaatctgtat actatcatgg gaaatcacat 300
 tataatcttaa ccttgtgggt ggagccactt gtcccctgac aatggtgcag aaacaagcag 360
 ccgcaaaaaa agctagaatc agccagtcct gcattcttgc ctgccaaatc atcatcttat 420
 tttctgcctc ttacatcagg tgcaacagct gcctgtgcag ggcaacgttc cagcccagggt 480
 tggggacctc ttggcgcccta gggaagatta agtcgacgcg gccgcgaatt caagcttact 540
 cttccttttt caattcanaa gaactcgtca agaangcgat agaaggcgat gcgctgcgaa 600
 tcggggagcgg cgatcccgtg aagcacgagg aagcggncag cccattcgcc gncaagctct 660
 tnaagcaatat cacgggtagc caacgctatg tncatgatagc n 701

<210> 284
 <211> 217
 <212> PRT
 <213> Mus musculus
 <220>
 <221> MOD_RES
 <222> (3)..(47)
 <223> XAA = ANYTHING

<400> 284
 Ala Ile Xaa Thr Arg Trp Leu Pro Val Ile Leu Leu Lys Ser Leu Xaa
 1 5 10 15
 Ala Asn Gly Leu Xaa Ala Ser Ser Cys Phe Thr Gly Ser Pro Leu Pro
 20 25 30
 Ile Arg Ser Ala Ser Pro Ser Ile Ala Phe Leu Thr Ser Ser Xaa Glu
 35 40 45
 Leu Lys Lys Glu Glu Ala Ile Arg Gly Arg Val Asp Leu Ile Phe Pro
 50 55 60

Arg Arg Gln Glu Val Pro Asn Leu Gly Trp Asn Val Ala Leu His Arg
 65 70 75 80
 Gln Leu Leu His Leu Met Glu Ala Glu Asn Lys Met Met Ile Trp Gln
 85 90 95
 Cys Lys Met Arg Asp Trp Leu Ile Leu Ala Phe Leu Ala Ala Ala Cys
 100 105 110
 Phe Cys Thr Ile Val Arg Gly Gln Val Ala Pro Pro Thr Arg Leu Arg
 115 120 125
 Tyr Asn Val Ile Ser His Asp Ser Ile Gln Ile Ser Trp Lys Ala Pro
 130 135 140
 Arg Gly Lys Phe Gly Gly Tyr Lys Leu Leu Val Ala Pro Ala Ser Gly
 145 150 155 160
 Gly Lys Thr Asn Gln Met Asn Leu Gln Asn Thr Ala Thr Lys Ala Ile
 165 170 175
 Ile Gln Gly Leu Leu Pro Glu Gln Asn Tyr Thr Val Gln Leu Ile Ala
 180 185 190
 Tyr Tyr Lys Asp Lys Glu Ser Lys Pro Ala Gln Gly Gln Phe Arg Ile
 195 200 205
 Lys Asp Leu Glu Lys Arg Asn Gly Ser
 210 215

<210> 285

<211> 723

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (600)..(707)

<223> N = A, C, G OR T/U

<400> 285

cttcgcatct tttactttca ccagcgtttc tgggtgggat ccgagcataa ataagacaga 60
 gaaaatccat ggatataagt attcttgcag gcaacaccac atagacattt agaaaattac 120
 ttaagtgttt tttgaatttt tactttacat gacttcatta attgtacttc cattaaagaa 180
 gagtttgtaa cacatctgta aacaaaaaag gcatatagca ttctattctt aatgaagaaa 240
 gaacatattt aaccacaaaag taaaggaata atcacataa aaagaagagc tttagctcat 300
 gaatatatat attgagttaa tgaataaata tatggtcgac gcggccgcga attcaagctt 360
 actcttcctt tttcaattca gaagaactcg tcaagaaggc gatagaaggc gatgcgctgc 420
 gaatcgggag cggcgatacc gtaaagcacg aggaagcggg cagcccattc gccgccaagc 480
 tcttcagcaa tatcacgggt agccaacgct atgtcctgat agcgggtccgc cacaccagc 540
 cggccacagt cgatgaatcc agaaaagcgg ccattttcca ccatgatatt cggcaagcan 600
 gcatcgccat gggtcacgac gagatcctcg ccgtcgggca tgcgcgcctt gagcctggcg 660
 aacagttcgg ctggcgcgag cccctgatgc tcttcgtcca gatcatnctg atcggaaga 720

<210> 286
 <211> 217
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (6)..(41)
 <223> XAA = ANYTHING

<400> 286

Arg Ser Cys Arg Ser Xaa Ser Gly Arg Arg Ala Ser Gly Ala Arg Ala
 1 5 10 15

Ser Arg Thr Val Arg Gln Ala Gln Gly Ala His Ala Arg Arg Arg Gly
 20 25 30

Ser Arg Arg Asp Pro Trp Arg Cys Xaa Leu Ala Glu Tyr His Gly Gly
 35 40 45

Lys Trp Pro Leu Phe Trp Ile His Arg Leu Trp Pro Ala Gly Cys Gly
 50 55 60

Gly Pro Leu Ser Gly His Ser Val Gly Tyr Pro Tyr Cys Arg Ala Trp
 65 70 75 80

Arg Arg Met Gly Pro Leu Pro Arg Ala Leu Arg Tyr Arg Arg Ser Arg
 85 90 95

Phe Ala Ala His Arg Leu Leu Ser Pro Ser Arg Val Leu Leu Asn Lys
 100 105 110

Arg Lys Ser Lys Leu Glu Phe Ala Ala Ala Ser Thr Ile Tyr Leu Phe
 115 120 125

Ile His Ser Ile Tyr Ile Phe Met Ser Ser Ser Ser Phe Tyr Cys Asp
 130 135 140

Tyr Ser Phe Thr Leu Trp Leu Asn Met Phe Phe Leu His Glu Asn Ala
 145 150 155 160

Ile Cys Leu Phe Cys Leu Gln Met Cys Tyr Lys Leu Phe Phe Asn Gly
 165 170 175

Ser Thr Ile Asn Glu Val Met Ser Lys Asn Ser Lys Asn Thr Val Ile
 180 185 190

Phe Met Ser Met Trp Cys Cys Leu Gln Glu Tyr Leu Tyr Pro Trp Ile
 195 200 205

Phe Ser Val Leu Phe Met Leu Gly Ser
 210 215

<210> 287
 <211> 705
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (655)
 <223> N = A, C, G OR T/U

<400> 287
 cttcagcatc ttttactttc accagcgttt ctgggtggga tccgggggtgt gttactggca 60
 tctatggagt agatgtaagt aatgttgata aacagcctat aatgcacagc atagcctgac 120
 ccccaaaaga agtatacatc ccagaatatac aatggtacag agattgagaa aactctcatt 180
 gagggcctag ttgtatttct tgttcaagac aagggttaca catttcaatt aagagagttc 240
 agctctacaa agaagtttta gtcgacgcgg ccgcgaattc aagcttactc ttcctttttc 300
 aattcagaag aactcgtcaa gaaggcgata gaaggcgatg cgctgcgaat cgggagcggc 360
 gataccgtaa agcacgagga agcggtcagc ccattcgccg ccaagctctt cagcaatatac 420
 acgggtagcc aacgctatgt cctgatagcg gtccgccaca cccagccggc cacagtcat 480
 gaatccagaa aagcggccat tttccaccat gatattcggc aagcaggcat cgccatgggt 540
 cagcagaga tcctcgccgt cgggcatgcy cgccttgagc ctggcgaaca gttcggctgg 600
 cgcgagcccc tgatgctctt cgtccagatc atcctgatcg acaaagaccg gcttncatcc 660
 gagtacgtgc tcgctcgatg cgatgtttcg cttgggtggc gaatg 705

<210> 288
 <211> 222
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (17)
 <223> XAA = ANYTHING

<400> 288
 Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met
 1 5 10 15

 Xaa Ala Gly Leu Cys Arg Ser Gly Ser Gly Arg Arg Ala Ser Gly Ala
 20 25 30

 Arg Ala Ser Arg Thr Val Arg Gln Ala Gln Gly Ala His Ala Arg Arg
 35 40 45

 Arg Gly Ser Arg Arg Asp Pro Trp Arg Cys Leu Leu Ala Glu Tyr His
 50 55 60

 Gly Gly Lys Trp Pro Leu Phe Trp Ile His Arg Leu Trp Pro Ala Gly
 65 70 75 80

 Cys Gly Gly Pro Leu Ser Gly His Ser Val Gly Tyr Pro Tyr Cys Arg
 85 90 95

Ala Trp Arg Arg Met Gly Pro Leu Pro Arg Ala Leu Arg Tyr Arg Arg
100 105 110

Ser Arg Phe Ala Ala His Arg Leu Leu Ser Pro Ser Arg Val Leu Leu
115 120 125

Asn Lys Arg Lys Ser Lys Leu Glu Phe Ala Ala Ala Ser Thr Lys Thr
130 135 140

Ser Leu Ser Thr Leu Leu Ile Glu Met Leu Pro Cys Leu Glu Gln Glu
145 150 155 160

Ile Gln Leu Gly Pro Gln Glu Phe Ser Gln Ser Leu Tyr His Tyr Ser
165 170 175

Gly Met Tyr Thr Ser Phe Gly Gly Gln Ala Met Leu Cys Ile Ile Gly
180 185 190

Cys Leu Ser Thr Leu Leu Thr Ser Thr Pro Met Pro Val Thr His Pro
195 200 205

Gly Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu
210 215 220

<210> 289

<211> 722

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (702)..(722)

<223> N = A, C, G OR T/U

<400> 289

cttcagcatc ttttactttc accagcgttt ctgggtggga tcccaggagt tttccttcgc 60
tgataaaggg ttctggaag caggtagcag cagagatggt acagacagca tctcccacat 120
agaaaatata cccattatc atcatttttc caaaacgagg ttcaatgggg agtttagcca 180
ggattcgtcc aagaggagtc aactcatcat tggcatctaa agcatcaagt tctcttagag 240
tatgctctgc ttcaattaca gcatccaaag gtggagggttc gattgccttt gcaaggaatt 300
ggccaattcc tcttagacgc agaagtttta tgctcagagc aatttcatgc aatggtgttc 360
taaacaatctc tgggtgcatg tgggtctcta gtctaaaatt tagaagtaga aaagtcaaac 420
atgacaacat aacaaaaatc tttgcataaa aaaactgggt attatagtgg ccctttccta 480
gtctatacca cacaactttt cctattgact acaaaaactag actagttgac tgaaaactgg 540
ctcctgactt tactttcaca gccagggtat cttttaactg ataagtagag gagtaaggaa 600
aaaagttaat gctaacactt ctaactatgg ctactaccta ccgacaccta ctattaacaa 660
gcacggacaa caacaaaacg ggcccaaact cagcaaaagg cnggacataa atataataaa 720
cn 722

<210> 290

<211> 237

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (7)

<223> XAA = ANYTHING

<400> 290

Val Tyr Tyr Ile Tyr Val Xaa Pro Phe Ala Glu Phe Gly Pro Val Leu
1 5 10 15

Leu Leu Ser Val Leu Val Asn Arg Asp Arg Val Val Ala Ile Val Arg
20 25 30

Ser Val Ser Ile Asn Phe Phe Pro Tyr Ser Ser Thr Tyr Gln Leu Lys
35 40 45

Asp Thr Leu Ala Val Lys Val Lys Ser Gly Ala Ser Phe Gln Ser Thr
50 55 60

Ser Leu Val Leu Ser Ile Gly Lys Val Val Trp Tyr Arg Leu Gly Lys
65 70 75 80

Gly His Tyr Asn Thr Gln Phe Phe Tyr Ala Lys Ile Phe Val Met Leu
85 90 95

Ser Cys Leu Thr Phe Leu Leu Leu Asn Phe Arg Leu Glu Thr His Met
100 105 110

Thr Pro Glu Met Phe Arg Thr Pro Leu His Glu Ile Ala Leu Ser Ile
115 120 125

Lys Leu Leu Arg Leu Gly Gly Ile Gly Gln Phe Leu Ala Lys Ala Ile
130 135 140

Glu Pro Pro Pro Leu Asp Ala Val Ile Glu Ala Glu His Thr Leu Arg
145 150 155 160

Glu Leu Asp Ala Leu Asp Ala Asn Asp Glu Leu Thr Pro Leu Gly Arg
165 170 175

Ile Leu Ala Lys Leu Pro Ile Glu Pro Arg Phe Gly Lys Met Met Ile
180 185 190

Met Gly Cys Ile Phe Tyr Val Gly Asp Ala Val Cys Thr Ile Ser Ala
195 200 205

Ala Thr Cys Phe Pro Glu Pro Phe Ile Ser Glu Gly Lys Leu Leu Gly
210 215 220

Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu
225 230 235

<210> 291

<211> 703
 <212> DNA
 <213> Mus musculus
 <220>
 <221> modified_base
 <222> (547)..(702)
 <223> N = A, C, G OR T/U

<400> 291
 cttcagcatc ttttactttc accagcgttt ctgggtggga tccactcttg ctacccaact 60
 gtttgtggaa gaaagtctgg agctgctgcc atgcgtccac ctgggccacg gcatgagccc 120
 tgggctcccc tccaaagggtg atgttggcac ccaccaggag gtgcatgcca gcgtgcaca 180
 gcgggaagta agggggctcg atgtaatgcc ctgctgctgg gtagcagatg atctggggct 240
 tctccttccc gtgcgcctgc aggcgtttgg agatctcatc agcatagaac tcgctcttcc 300
 agttgtggtc gtcctgacct acgaggaaca ggaaggctcg gtcagacctt tccacgggaa 360
 tgaagctctt cttgtctacc agagggttt gcagagcttc cagcacatcc aagagaccat 420
 ctttggatcat tttgacttgg tttctcagaa gggacacagg gggatatagc tcaccttctg 480
 aggagatggt gttcccaaca gcagccacgg agccattgat gaccacagca gctgtgatgc 540
 ccttcangaa ggaggccata ncaaggccaa gttcaccccc tttggaaatc ccaagcagcc 600
 caattccagg tccttttacc tcggggtggc tgcgcangta gttcacggct tcttcaaagt 660
 actccatgtg catgggttct atgctcttgg ggaaggctcg cnt 703

<210> 292
 <211> 703
 <212> DNA
 <213> Mus musculus
 <220>
 <221> modified_base
 <222> (695)
 <223> N = A, C, G OR T/U

<400> 292
 cttcagcatc ttttactttc accagcgttt ctgggtggga tccactcttg ctacccaact 60
 gtttgtggaa gaaagtctgg agctgctgcc atgcgtccac ctgggccacg gcatgagccc 120
 tgggctcccc tccaaagggtg atgttggcac ccaccaggag gtgcatgcca gcgtgcaca 180
 gcgggaagta agggggctcg atgtaatgcc ctgctgctgg gtagcagatg atctggggct 240
 tctccttccc gtgcgcctgc aggcgtttgg agatctcatc agcatagaac tcgctcttcc 300
 agttgtggtc gtcctgacct acgaggaaca ggaaggctcg gtcagacctt tccacgggaa 360
 tgaagctctt cttgtctacc agagggttt gcagagcttc cagcacatcc aagagaccat 420
 ctttggatcat tttgacttgg tttctcagaa gggacacagg gggatatagc tcaccttctg 480
 aggagatggt gttcccaaca gcagccacgg agccattgat gaccacagca gctgtgatgc 540
 ccttcaggaa ggaggccata gcaaggccaa gttcaccccc tttggaaatc ccaagcagcc 600
 caattccagg tccttttacc tcggggtggc tgcgcaggta gttcacggct tcttcaaaag 660
 tactccatgt gcatgggtttc tatgctcttg gggangtctg cgt 703

<210> 293
 <211> 231
 <212> PRT
 <213> Mus musculus

<400> 293

Thr Ser Pro Arg Ala Lys Pro Cys Thr Trp Ser Thr Phe Glu Glu Ala
 1 5 10 15
 Val Asn Tyr Leu Arg Ser His Pro Glu Val Lys Gly Pro Gly Ile Gly
 20 25 30
 Leu Leu Gly Ile Ser Lys Gly Gly Glu Leu Gly Leu Ala Met Ala Ser
 35 40 45
 Phe Leu Lys Gly Ile Thr Ala Ala Val Val Ile Asn Gly Ser Val Ala
 50 55 60
 Ala Val Gly Asn Thr Ile Ser Tyr Lys Asp Glu Thr Ile Pro Pro Val
 65 70 75 80
 Ser Leu Leu Arg Asn Gln Val Lys Met Thr Lys Asp Gly Leu Leu Asp
 85 90 95
 Val Val Glu Ala Leu Gln Ser Pro Leu Val Asp Lys Lys Ser Phe Ile
 100 105 110
 Pro Val Glu Arg Ser Asp Thr Thr Phe Leu Phe Leu Val Gly Gln Asp
 115 120 125
 Asp His Asn Trp Lys Ser Glu Phe Tyr Ala Asp Glu Ile Ser Lys Arg
 130 135 140
 Leu Gln Ala His Gly Lys Glu Lys Pro Gln Ile Ile Cys Tyr Pro Ala
 145 150 155 160
 Ala Gly His Tyr Ile Glu Pro Pro Tyr Phe Pro Leu Cys Ser Ala Gly
 165 170 175
 Met His Leu Leu Val Gly Ala Asn Ile Thr Phe Gly Gly Glu Pro Arg
 180 185 190
 Ala His Ala Val Ala Gln Val Asp Ala Trp Gln Gln Leu Gln Thr Phe
 195 200 205
 Phe His Lys Gln Leu Gly Ser Lys Ser Gly Ser His Pro Glu Thr Leu
 210 215 220
 Val Lys Val Lys Asp Ala Glu
 225 230

<210> 294

<211> 623

<212> DNA

<213> Mus musculus

<400> 294

gaattcgcgg ccggcgtcga cgaaacagga tctcccttct ctgctcagag atgagcaaat 60
 gccataatta cgacctcaag ccagcaaaagt gggatacttc tcaagaacaa cagaaacaaa 120
 gattagcact aactaccagt caacctggag aaaatggtat cataagagga agatacccta 180

```

tagaaaaact caaaatatct ccaatgttcg ttgttcgagt ccttgctata gccttggcaa 240
ttcgattcac ccttaacaca ttgatgtggc ttgccatttt caaagagacg tttcagccag 300
tattgtgcaa caaggaagtc ccagtttcct caagagaggg ctactgtggc ccatgcccta 360
acaactggat atgtcacaga aacaactgtt accaattttt taatgaagag aaaacctgga 420
accagagcca agcttcctgt ttgtctcaaa attccagcct tctgaagata tacagtaaag 480
aagaacagga tttcttaaag ctggttaagt cctatcactg gatgggactg gtccagatcc 540
cagcaaatgg ctctctggcag tgggaagatg gtcctctct ctcatacaat cagttaactc 600
tggtggaaat accaaaagga tcc 623

```

```

<210> 295
<211> 226
<212> PRT
<213> Mus musculus

```

```

<220>
<221> MOD_RES
<222> (17)
<223> XAA = ANYTHING

```

```

<400> 295
Ala Ser Pro Ser Ile Ala Phe Leu Thr Ser Ser Ser Glu Leu Lys Lys
  1             5             10             15

Xaa Glu Ala Ile Arg Gly Arg Arg Arg Arg Asn Arg Ile Ser Leu Leu
      20             25             30

Cys Ser Glu Met Ser Lys Cys His Asn Tyr Asp Leu Lys Pro Ala Lys
      35             40             45

Trp Asp Thr Ser Gln Glu Gln Gln Lys Gln Arg Leu Ala Leu Thr Thr
      50             55             60

Ser Gln Pro Gly Glu Asn Gly Ile Ile Arg Gly Arg Tyr Pro Ile Glu
      65             70             75             80

Lys Leu Lys Ile Ser Pro Met Phe Val Val Arg Val Leu Ala Ile Ala
      85             90             95

Leu Ala Ile Arg Phe Thr Leu Asn Thr Leu Met Trp Leu Ala Ile Phe
      100            105            110

Lys Glu Thr Phe Gln Pro Val Leu Cys Asn Lys Glu Val Pro Val Ser
      115            120            125

Ser Arg Glu Gly Tyr Cys Gly Pro Cys Pro Asn Asn Trp Ile Cys His
      130            135            140

Arg Asn Asn Cys Tyr Gln Phe Phe Asn Glu Glu Lys Thr Trp Asn Gln
      145            150            155            160

Ser Gln Ala Ser Cys Leu Ser Gln Asn Ser Ser Leu Leu Lys Ile Tyr
      165            170            175

Ser Lys Glu Glu Gln Asp Phe Leu Lys Leu Val Lys Ser Tyr His Trp

```

180 185 190
 Met Gly Leu Val Gln Ile Pro Ala Asn Gly Ser Trp Gln Trp Glu Asp
 195 200 205

Gly Ser Ser Leu Ser Tyr Asn Gln Leu Thr Leu Val Glu Ile Pro Lys
 210 215 220

Gly Ser
 225

<210> 296
 <211> 317
 <212> DNA
 <213> Mus musculus

<400> 296
 gaattcgcgg ccgcgtcgac cagctgtgtg ctgccctgct tctgctcaac ctgatcttcc 60
 tcctagactc ctggattgcg ctgtataata cccgagggtt ctgcattgcc gtggctgtat 120
 ttcttcacta ttttctcttg gtctcattca catggatggg attagaagca ttccacatgt 180
 acctagcact ggtcaagggtg ttttaatactt acatccgaaa gtacatcctt aaattctgca 240
 ttgttggtg gggcatacca gctgtgggtg tgtccatcgt cctgactata tccccagata 300
 actatgggat tggatcc 317

<210> 297
 <211> 232
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (2)..(23)
 <223> XAA = ANYTHING

<400> 297
 Ile Xaa Thr Lys Ser Ile Arg Gly Ser Arg Gln Pro Asn Cys Ser Pro
 1 5 10 15

Gly Ser Arg Arg Ala Cys Xaa Thr Ala Arg Ile Ser Ser Pro Met Ala
 20 25 30

Met Pro Ala Cys Arg Ile Ser Trp Trp Lys Met Ala Ala Phe Leu Asp
 35 40 45

Ser Ser Thr Val Ala Gly Trp Val Trp Arg Thr Ala Ile Arg Thr Arg
 50 55 60

Trp Leu Pro Val Ile Leu Leu Lys Ser Leu Ala Ala Asn Gly Leu Thr
 65 70 75 80

Ala Ser Ser Cys Phe Thr Val Ser Pro Leu Pro Ile Arg Ser Ala Ser
 85 90 95

Pro Ser Ile Ala Phe Leu Thr Ser Ser Ser Glu Leu Lys Lys Glu Glu
100 105 110

Ala Ile Arg Gly Arg Val Asp Gln Leu Cys Ala Ala Leu Leu Leu Leu
115 120 125

Asn Leu Ile Phe Leu Leu Asp Ser Trp Ile Ala Leu Tyr Asn Thr Arg
130 135 140

Gly Phe Cys Ile Ala Val Ala Val Phe Leu His Tyr Phe Leu Leu Val
145 150 155 160

Ser Phe Thr Trp Met Gly Leu Glu Ala Phe His Met Tyr Leu Ala Leu
165 170 175

Val Lys Val Phe Asn Thr Tyr Ile Arg Lys Tyr Ile Leu Lys Phe Cys
180 185 190

Ile Val Gly Trp Gly Ile Pro Ala Val Val Val Ser Ile Val Leu Thr
195 200 205

Ile Ser Pro Asp Asn Tyr Gly Ile Gly Ser His Pro Glu Thr Leu Val
210 215 220

Lys Val Lys Asp Ala Glu Asp Gln
225 230

<210> 298

<211> 686

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (5)

<223> N = A, C, G OR T/U

<400> 298

tcttntagtt tgacaggcaa catcccaaaa actttttcgaa gcatttgttc agatcttcag 60
tattttccag ttttcataca gtctcggggt ttcaaaacgt tgaaatcaag gacacgacgt 120
ttgcagtcta cctctgaaag attagtagaa gcacagaata tagcccatca tttgtgaagg 180
ggttttctttt gcgggacaga ggaacagatc ttgagagttt ggacaaaactt atgaaaacta 240
aaaacatacc tgaagctcac caagatgcat ttaaaaactgg ttttgcagag ggtttttctca 300
aagctcaagc tcttacacag aagaccaatg attccttaag gcgaactcgt ctgacacctt 360
ttgtttttgct cctgtttggc atttatggac tcttaaaaaa tccgttttta tctgtgcgct 420
ttcggacaac tacaggactt gattctgcgg tagaccctgt ccagatgaaa aatgtcactt 480
ttgaacatgt taaaggggtg gaggaagcca aacaagagtt acaggaagtg gttgaattct 540
tgaaaaatcc acagaagttt actgtgcttg gaggtaaact tcccaaagga attcttttag 600
ttggggccacc aggaacaggg aagacgcttc ttgcccagac tgtggcagga gaagctgacg 660
tcccttttta ttatgcttct ggatcc 686

<210> 299

<211> 237

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (1)

<223> XAA = ANYTHING

<400> 299

Xaa Phe Asp Arg Gln His Pro Lys Asn Phe Ser Lys His Leu Phe Arg
1 5 10 15

Ser Ser Val Phe Ser Ser Phe His Thr Val Ser Gly Phe Gln Asn Val
20 25 30

Glu Ile Lys Asp Thr Thr Phe Ala Val Tyr Leu Lys Ile Ser Arg Ser
35 40 45

Thr Glu Tyr Ser Pro Ser Phe Val Lys Gly Phe Leu Leu Arg Asp Arg
50 55 60

Gly Thr Asp Leu Glu Ser Leu Asp Lys Leu Met Lys Thr Lys Asn Ile
65 70 75 80

Pro Glu Ala His Gln Asp Ala Phe Lys Thr Gly Phe Ala Glu Gly Phe
85 90 95

Leu Lys Ala Gln Ala Leu Thr Gln Lys Thr Asn Asp Ser Leu Arg Arg
100 105 110

Thr Arg Leu Ile Leu Phe Val Leu Leu Leu Phe Gly Ile Tyr Gly Leu
115 120 125

Leu Lys Asn Pro Phe Leu Ser Val Arg Phe Arg Thr Thr Thr Gly Leu
130 135 140

Asp Ser Ala Val Asp Pro Val Gln Met Lys Asn Val Thr Phe Glu His
145 150 155 160

Val Lys Gly Val Glu Glu Ala Lys Gln Glu Leu Gln Glu Val Val Glu
165 170 175

Phe Leu Lys Asn Pro Gln Lys Phe Thr Val Leu Gly Gly Lys Leu Pro
180 185 190

Lys Gly Ile Leu Leu Val Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu
195 200 205

Ala Arg Ala Val Ala Gly Glu Ala Asp Val Pro Phe Tyr Tyr Ala Ser
210 215 220

Gly Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala
225 230 235

<210> 300
 <211> 705
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (655)
 <223> N = A, C, G OR T/U

<400> 300
 cttcagcatc ttttactttc accagcgttt ctgggtggga tccggggtgt gttactggca 60
 tctatggagt agatgtaagt aatgttgata aacagcctat aatgcacagc atagcctgac 120
 cccaaaaga agtatacatc ccagaatatc aatggtacag agattgagaa aactctcatt 180
 gagggcctag ttgtatttct tgttcaagac aaggttacia catttcaatt aagagagttc 240
 agctctacaa agaagtttta gtcgacgcgg ccgcgaattc aagcttactc ttccctttttc 300
 aattcagaag aactcgtcaa gaaggcgata gaaggcgatg cgctgcgaat cgggagcggc 360
 gataccgtaa agcacgagga agcggtcagc ccattcgccg ccaagctctt cagcaatata 420
 acgggtagcc aacgctatgt cctgatacgc gtccgccaca cccagccggc cacagtcgat 480
 gaatccagaa aagcggccat tttccaccat gatattcggc aagcaggcat cgccatgggt 540
 cacgacgaga tcctcgccgt cgggcatgcg cgccttgagc ctggcgaaca gttcggctgg 600
 cgcgagcccc tgatgctctt cgtccagatc atcctgatcg acaaagaccg gcttncatcc 660
 gagtacgtgc tcgctcgatg cgatgtttcg cttgggtggc gaatg 705

<210> 301
 <211> 723
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (600)..(707)
 <223> N = A, C, G OR T/U

<400> 301
 cttcgcacat tttactttca ccagcgtttc tgggtgggat ccgagcataa ataagacaga 60
 gaaaatccat ggatataagt attcttgacg gcaacaccac atagacattt agaaaattac 120
 ttaagtgttt tttgaatttt tactttacat gacttcatta attgtacttc cattaaagaa 180
 gagtttgtaa cacatctgta aacaaaaaag gcatatagca ttctattctt aatgaagaaa 240
 gaacatattt aaccacaaag taaaggaata atcacaataa aaagaagagc tttagctcat 300
 gaatatatat attgagtga tgaataaata tatggtcgac gcggccgga attcaagctt 360
 actcttcctt tttcaattca gaagaactcg tcaagaaggc gatagaaggc gatgcgctgc 420
 gaatcgggag cggcgatacc gtaaagcacg aggaagcggg cagcccatc gcgcgaagc 480
 tcttcagcaa tatcagggg agccaacgct atgtcctgat agcggtcgac cacaccagc 540
 cggccacagt cgatgaatcc agaaaagcgg ccattttcca ccatgatatt cggcaagcan 600
 gcatcgccat ggggtcacgac gagatcctcg ccgtcgggca tgcgcgcctt gagcctggcg 660
 aacagttcgg ctggcgcgag cccctgatgc tcttcgtcca gatcatnctg atcggcaaga 720
 ccg 723

<210> 302
 <211> 610
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (495)..(571)
 <223> N = A, C, G OR T/U

<400> 302
 ggatccacag agtgcgggggt cccctgccac cactttcttg gagcttttct ctgtagtacc 60
 caggagcaca gtcctgacag gagtgtcctg cggtgccagg aggacagaca cagagctcca 120
 acagcaatgc cgcctcgccc tcagcgggca gctcgacagc tttccggcca acctccatgg 180
 aaatgttggc aattctgctc tgctgcagtc cctggcgcta tgatgctttg atgaggatgt 240
 agtcaatatt gctgagaaca gacataaaat cagagtgtgt gacgtgtttc tcagacacgg 300
 agttaaataa tttccagaat tcaagcttac tcttcctttt tcaattcaga agaactcgtc 360
 aagaaggcga tagaaggcga tgcgctgcga atcgggagcg gcgataccgt aaagcacgag 420
 gaagcggta gcccattcgc cgccaagctc ttcagcaata tcacgggtag ccaacgctat 480
 gtcctgatag cggtncgcca caccagccg gccacagtcg atgaatccag aaaagcggtc 540
 attttccacc atgatattcg gcaagcagcg ntcgccatgg gtcacgacga agatcctcgc 600
 ccgtccggcg 610

<210> 303
 <211> 606
 <212> DNA
 <213> Mus musculus

<400> 303
 ggatcccaat acttcgacca ggtgaccccc tggtaaattgt gtgtaagaca tctacaaaat 60
 cagcgtcatc aggagaaagg cgactggggg cttctgcata ctcaaagtta ggcccagctg 120
 gatccgaaca accataacca tccagaaatt ttcttctggt tcattgaaga actgtctgtt 180
 cttctgtgtg tgtaaagatt ttgcaggttt cgatgggcta aaagtccttg taaactgtac 240
 aattgcttca cataatccaa catttctaatt tttttcattc ttttctactt catttgatg 300
 gtaaaacaga attttatttt cttcctctcc cccgcggggc cgaattcaag cttactcttc 360
 ctttttcaat tcagaagaac tcgtcaagaa ggcgatagaa ggcgatgcgc tgcaaatcgg 420
 gagcggcgat accgtaaagc acgaggaagc ggtcagccca ttcgcccga agctcttcag 480
 caatatcacg ggtagccaac gctatgtcct gatagcggtc cgccacaccc agccggccac 540
 agtcgatgaa tccagaaaag cggccatttt ccaccatgat attcggcaag caggcatcgc 600
 catggg 606

<210> 304
 <211> 608
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (589)
 <223> N = A, C, G OR T/U

<400> 304
 ggatcccaat cctgctgctg gagtgtcttc gcaaaccctt gctgtcgctt ggaaaaaagt 60
 gcccaagctg ctgacgcaaa aagaaaaaaa aaaagaaaga aagatgctgc tcatttgcatt 120
 gctcacttac atatatttgc atgttacttg acccagcctg agctctcccc agcctcgtgg 180
 gtgggtgactt ttcctgcagg gcgcacgccc tgctgcagcc ccctcccccg cggggccgaa 240
 ttcaagctta ctcttccttt ttcaattcag aagaactcgt caagaaggcg atagaaggcg 300

```

atgcgctgcg aatcgggagc ggcgataccg taaagcacga ggaagcggtc agcccattcg 360
ccgccaagct cttcagcaat atcacgggta gccaacgcta tgtcctgata gcgggtccgcc 420
acaccagacc ggccacagtc gatgaatcca gaaaagcggc cattttccac catgatattc 480
ggcaagcagg catcgccatg ggtcacgacg agatcctcgc cgtcggggcat gcgcgccttg 540
agcctggcga acagttcggc tggcgcgagc ccctgatgct cttcgtcana tcatcctgat 600
cgacaagg                                         608

```

<210> 305

<211> 635

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (596)..(635)

<223> N = A, C, G OR T/U

<400> 305

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ggatcccaat cctgctgctg gagtgtcttc gcaaacccct gctgtcgcct ggaaaaaagt 60
gcccaagctg ctgacgcaaa aagaaaaaaa aaaagaaaga aagatgctgc tcatttgcac 120
gtcacttac atatatattg atgttactg acccagcctg agctctcccc agcctcgtgg 180
gtggtgactt ttcttcgagg gcgcacgccc tgctgcagcc ccctcccccg cggggccgaa 240
ttcaagctta ctcttccttt ttcaattcag aagaactcgt caagaaggcg atagaaggcg 300
atgcgctgcg aatcgggagc ggcgataccg taaagcacga ggaagcggtc agcccattcg 360
ccgccaagct cttcagcaat atcacgggta gccaacgcta tgtcctgata gcgggtccgcc 420
acaccagacc ggccacagtc gatgaatcca gaaaagcggc cattttccac catgatattc 480
ggcaagcagg catcgccatg ggtcacgacg agatcctcgc cgtcggggcat gcgcgccttg 540
agcctggcga acagttcggc tggcgcgagc ccctgatgct cttcgtccag atcatnctga 600
tcgacaagac cggctttcat tccgagtacg tgctn                                         635

```

<210> 306

<211> 635

<212> DNA

<213> Mus musculus

<400> 306

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ggatcccacg gggaaaggtg gcacagggtg tattgtggaa tgccacggac ccggtgtcga 60
ttccatctcc tgcactggca tggcaactat ctgcaacatg ggtgcagaaa ttggggccac 120
tacatcagtg ttcccatata accacaggat gaaaaagtac ctgagcaaga caggccgaac 180
agacattgcc aacctagcag aagaattcaa gcttactctt cttttttcaa ttcagaagaa 240
ctcgtcaaga aggcgataga aggcgatgcy ctgcgaatcg ggagcggcga taccgtaaaag 300
cacgaggaag cggtcagccc attcgcggcc aagctcttca gcaatatcac gggtagccaa 360
cgctatgtcc tgatagcggc ccgccacacc cagccggcca cagtcgatga atccagaaaa 420
gcggccattt tccaccatga tattcgccaa gcaggcatcg ccatgggtca cgacgagatc 480
ctcgcgctcg ggcgatgcgc ccttgagcct ggccaacaag ttcggctggc gcgagcccct 540
gatgtctctt gtccagatca tctgatcga caaagaccgg ctttcatccg agtacctgct 600
cgctcgatgc gatgtttcct tggggggcga atggg                                         635

```

<210> 307

<211> 635

<212> DNA

<213> Mus musculus

<400> 307

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ggatccctcg gtgaaagggtg gcacagggtgc tattgtggaa taccacggac ccggtgtcga 60
ttccatctcc tgcactggca tggcaactat ctgcaacatg ggtgcagaaa ttggggccac 120
tacgtcagtg ttcccataca accacaggat gaaaaagtag ctgagcaaga caggccgaac 180
agacattgcc aacctagcag aagaattcaa gcttactctt cctttttcaa ttcagaagaa 240
ctcgtcaaga aggcgataga aggcgatgcg ctgcgaatcg ggagcggcga taccgtaaag 300
cacgaggaag cggtcagccc attcgcgcgc aagctcttca gcaatatcac gggtagccaa 360
cgctatgtcc tgatagcggg ccgccacacc cagccggcca cagtcgatga atccagaaaa 420
gcggccattt tccaccatga tattcggcaa gcaggcatcg ccatgggtca cgacgagatc 480
ctcgccgctcg ggcattgcgc ccttgagcct ggccaacagt tcggctggcg cgagcccctg 540
atgctcttcg tccagatcat cctgatcgac aagaccggct ttcattccga gtacgtgctc 600
gctcgatgcg atgtttcgct tgggtggtcga atggg 635
```

<210> 308

<211> 635

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (524)

<223> N = A, C, G OR T/U

<400> 308

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ggatccctgc ggccactgcc cagagagaat cgttacaatc acaggcccaa ctgacgccat 60
cttcaaggcc tttgctatga tcgcgtacaa gtttgaggag gacatcatta attccatgag 120
caacagcccc gccccgcggg gcccgaaatc aagcttactc ttcctttttc aattcagaag 180
aactcgtcaa gaaggcgata gaaggcgatg cgctgcgaat cgggagcggc gataccgtaa 240
agcacgagga agcggtcagc ccattgcgcg ccaagctctt cagcaatatc acgggtagcc 300
aacgctatgt cctgatagcg gtccgccaca cccagccggc cacagtcgat gaatccagaa 360
aagcggccat tttccaccat gatattcggc aagcaggcat cgccatgggt cacgacgaga 420
tctcgcctgt cgggcatgcg cgccttgagc ctggcgaaca gttcggctgg cgcgagcccc 480
tgatgctctt cgtccagatc atcctgatcg acaagaccgg cttncatccg agtacgtgct 540
cgctcgatgc gatgtttcgc ttggtggtcg aatgggcagg tagccggatc aaagcgtatg 600
cagcccgcgc cattgcatca gccatgatgg atact 635
```

<210> 309

<211> 631

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (580) .. (597)

<223> N = A, C, G OR T/U

<400> 309

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ggatccgaca ccgtcttctg gcttccacag gcgcccattc acaatgtgtg gcacacatat 60
ctagaaacat agacatatga agaaaataaa aataactcgg tagagctggg cattgtggta 120
catattttta gtcctagcat ttgggagaca acagaaagcg gagcgtgtg gggtcaaate 180
tagcctgatc cacatgggtg gtgagttcta ggccaaccga ggatgagAAC ttgtctcaaa 240
acagttttta aagaaaatac tctagaataa aacagaacta agcaccacca ccagtagagt 300
```

```

gcacagaaat aagacacact ggtgctgaat atttcatagc ctgtgtgtgt ctgtccttcc 360
tttcctttat gttttttttt gagacagggt ttctctgtgt agccctgggt gttctggaac 420
tcaactctgta gaccatgctg gcctcaaact cagaaatttg cctgcctctg cctcccaagt 480
gctgaaatga aagggtgtgtg cactacgtgt ttcttttctt ttttaattaac taattaatta 540
acatctcaaa cactggctcc cccttcgtgg taccctctn acagagtccc ttccctnccc 600
tctttctttc tcctgtgaga gtgtgcccgc g 631

```

<210> 310

<211> 603

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (512)..(597)

<223> N = A, C, G OR T/U

<400> 310

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ggatccgacc ccctgccgtt ctctatgtgc ttctatgagg gttactatga tgaaaataga 60
gcagaagata gtgtgaagta acattggcaa ctgtaatgtg tccatttaac ttatttttat 120
agcacttagg caatattgtt agtcttagtg agtagttcac atctttacaa aagcatgctc 180
tccctatcca ttgggcccac aataacactc tctttgaggc cattctgaat cctgtctcgt 240
gtaacgataa tatattatga aaacagatac tttagaatt tcctgtacag cagtcagttg 300
tttattctct ctctctctct ctctctctct ctctctctct ctctctctct ccctcgggcc 360
caatcccgcg ggcctgaatt caagcttact ctctctttt caattcagaa gaactcgtca 420
agaaggcgat agaaggcgat gcgctgcgaa tcgggagcgg cgataccgta aagcacgagg 480
aagcggtcag cccattcgcc gccaaagctc tnaagcaat cagcggtagc caacgctatg 540
tcctgatagc ggccgncaca ccagccgggn cacagtcgat gaatccagaa aagcggncat 600
ttt 603

```

<210> 311

<211> 608

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (489)..(596)

<223> N = A, C, G OR T/U

<400> 311

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ggatccgcat ggcattgata cgatttggaa cattgcaacc aacaagctga ccttcctcaa 60
ctccttcaag atgaagatgt ctgttatcct cggcatcatc cacatgctgt ttggagtcag 120
cctgagcctt ttcaaccata tctatttcaa gaagcccctg aacatctact ttggctttat 180
tcctgagatc atcttcatgt cctcgttgtt tggtacactg gtcacctta tcttttacia 240
gtggacagcc tacgatgcc actcgtctag gaatgcccc agcctcctga tccacttcat 300
aaacatgttc ctcttctct acccagagtc tggtaatgca atgctgtact ctggacagaa 360
aggaattcaa gcttactctt cctttttcaa ttcagaagaa ctctcaaga aggcgataga 420
aggcgatgag ctgcgaatcg ggagcggcga taccgtaaag cacgaggaag cggtcagccc 480
attcgccgnc aagctctttc agcaatatca cgggtagcca acgctatgtc ctgatagcgg 540
gccgccacac ccagccgggc acaggtcgat gaattcagaa aagcgggcca tttttncacc 600
atgatatt 608

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<210> 312
 <211> 637
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (117)..(627)
 <223> N = A, C, G OR T/U

<400> 312
 ggatccgccg ggggtcagaa gccatggagt cagcattatc accaaggata ttattgaata 60
 cccaaataaa acgaactgat acatatttct ccaaaacctt cacaagaagt cgactgnttt 120
 ctttagtagg ctaacttttt aaacattcca caagaggaag tgcccgcggg cctgaattca 180
 agcttactct tcctttttca attcagaaga actcgtcaag aaggcgatag aaggcgatgc 240
 gctgcgaatc gggagcggcg ataccgtaaa gcacgaggaa gcggtcagcc cattcgccgc 300
 caagctcttc agcaatatca cgggtagcca acgctatgtc ctgatatcgg tccgccacac 360
 ccagccggcc acagtcgatg aatncagaaa agcggncatt ttccaccatg atattcggca 420
 acgaggcatc gccatgggtc acgacgagat cctcgccgtc gggcatgcgc gccttgagcc 480
 tggcgaacag ttcgggtggc gcgagccctt gatgctcttc gtccagatca tctgatcga 540
 caaagaccgg nttncatccg agtaccgtgc tcgctcgatg cgangtttcg cttggnggtn 600
 naatgggcag gttagnccgg atcaagngta tgcagcc 637

<210> 313
 <211> 607
 <212> DNA
 <213> Mus musculus

<400> 313
 ggatccggca ggaagaggcc aggcagatgc agaagcagca gcagcagcaa caacaacaac 60
 aacagcaaca ccagcaatca aacagagccc ggaacagcac acattccaac ctgcatacca 120
 gccttgggaa ttcaagctta ctcttccttt ttcaattcag aagaactcgt caagaaggcg 180
 atagaaggcg atgcgctgcg aatcgggagc ggcgataccg taaagcacga ggaagcggtc 240
 agcccattcg ccgccaagct cttcagcaat atcacgggta gccaacgcta tgtcctgata 300
 gcggtccgcc acaccagcc ggccacagtc gatgaatcca gaaaagcggc ctttttccac 360
 catgatattc ggcaagcagg catcgccatg ggtcacgacg agatcctcgc cgtcgggcat 420
 gcgcgccttg agcctggcga acagttcggc tggcgcgagc ccctgatgct cttcgtccag 480
 atcatcctga tcgacaagac cggcttcatc cgagtacgtg ctcgctcgat gcgatgtttc 540
 gcttggtggt cgaatgggca ggtagccgga tcaagcgtat gcagccgccg cattgcatca 600
 gccatga 607

<210> 314
 <211> 633
 <212> DNA
 <213> Mus musculus

<400> 314
 ggatccggtc agaagccatg gagtcagcat tatcaccaag gatattattg aatacccaaa 60
 taaaacgaac tgatacatat ttctccaaa ccttcacaag aagtcgactg ttttctttag 120
 taggtaact ttttaaacat tccacaagag gaagggcccgc cgggcccga tccaagctta 180
 ctcttccttt ttcaattcag aagaactcgt caagaaggcg atagaaggcg atgcgctgcg 240
 aatcgggagc ggcgataccg taaagcacga ggaagcggtc agcccattcg ccgccaagct 300

```

cttcagcaat atcacgggta gccaacgcta tgtcctgata gcggtccgcc acacccagcc 360
ggccacagtc gatgaatcca gaaaagcggc cttttccac catgatattc ggcaagcagg 420
catcgccatg ggtcacgacg agatcctcgc cgtcgggcat gcgcgccttg agcctggcga 480
acagttcggc tggcgcgagc ccctgatgct cttcgtccag atcatcctga tcgacaagac 540
cggtctccat ccgagtacgt gctcgtcga tgcgatgttt cgcttggtgg tcgaatgggc 600
aggtagccgg atcaagcgta tgcagccgc cgc 633

```

<210> 315

<211> 631

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (7)..(631)

<223> N = A, C, G OR T/U

<400> 315

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ggatccnttg ngggnnatna ccnnnggagn naccatnatn annaaggata tnatatgaat 60
accaagatc attggncntg atgngtatgt tctnnacaac ctntatatga ancagactgc 120
nnmntntnat mngcnaantt nnnaanngtt acncaagang aantgtccnt tnnccnatat 180
tcaagntnnc tnttcntttg tnantrnaagn ngancnctg nanatngcga ncgaaggtn 240
ngcgctgcnn annngnancg gcnatccctt nnannacgag gnatnggnca gtctattngc 300
nggccanctc tttntcntna tnnccggctg ccannnctat gngctnanag cggatnnana 360
cacncangcg gccannntcc atnatnanat nnnngcggcc nttntccacc nngatntnna 420
nnagnnnctc atcgatcatg ntgcnacctn ntccctggcg accngcatgc gctgctngag 480
ccngtgatnc agttcggctg gancnnngctn ntgangctgt tcgncntgan tatcctganc 540
nacatgatcg gtnngatgcn agttcngct cgctntntgc gatgtttccg ttgaaggntc 600
antgggcngg tnnattggat caagccattg n 631

```

<210> 316

<211> 607

<212> DNA

<213> Mus musculus

<400> 316

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ggatcctaac ctcacagctg aaagcagcca tagcagaatg caggccagag aacgaacttt 60
agaaataacc cacctacttg tgtctgggga attcaagctt actcttcctt tttcaattca 120
gaagaactcg tcaagaaggc gatagaaggc gatgcgctgc gaatcgggag cggcgatacc 180
gtaaagcacg aggaagcggg cagcccatc gccgccaagc tcttcagcaa tatcacgggt 240
agccaacgct atgtcctgat agcggccgc cacaccagc cggccacagt cgatgaatcc 300
agaaaagcgg ccattttcca ccatgatatt cggcaagcag gcatcgccat gggtcacgac 360
gagatcctcg ccgtcgggca tgcgcgcctt gagcctggcg aacagttcgg ctggcgcgag 420
cccctgatgc tcttcgtcca gatcatcctg atcgacaaga ccggcttcca tccgagtacg 480
tgctcgtcgt atgcgatgtt tcgcttggtg gtcgaatggg caggtagccg gatcaagcgt 540
atgcagccgc cgcattgcat cagccatgat ggatactttc tcggcaggag caaggtggga 600
tgacagg 607

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<210> 317

<211> 225

<212> DNA

<213> Mus musculus

<220>
 <221> modified_base
 <222> (13)..(204)
 <223> N = A, C, G OR T/U

<400> 317
 ggatcctcac tgnncggcaa aatgccgcaa aaaaggggaat aagggcgaca cggaatgtt 60
 gaatactcat actcttcctt tttcaatatt attgaagcat ttatcagggt tattgtctca 120
 tgagcggata catatattgaa tgtattctgc agaagaacat gtgagcaaaa ggccagcnaa 180
 aggccntnan ccggaaaaaag gccncgctgc tggctttttt ccata 225

<210> 318
 <211> 633
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (8)..(630)
 <223> N = A, C, G OR T/U

<400> 318
 ggatcctnac tgnncggcaa ancgccgcaa aaaaggggaat gggggctgac acgganatgt 60
 ttgaatactc atactcttcc tttnttanta ttnttgaann nttntcnng nntattggnt 120
 natgagcggg tacntatttg aatgtattct gcataagaac atgtgagcaa aaggccagca 180
 naaggccngg aaccggaaaa aggccnggtt gctggcggtt ttccataggc tccgaccccc 240
 tgacgagcat canaaaaatc gacgctcaat tcagatgtgg caaaccgcac tggactataa 300
 agataccagg cgtttacccc tgnnanctcc ctagnccgct ntctgttnc gncctgccc 360
 cttaccggat acctgtccgc ctttctccct tcgggaagcg tggcgctttc tcatagctca 420
 cgctgtatgt ntctcangtc ggtgtaggta ngntcgctcc aatctgggct gngtgcacga 480
 accncgcgtt cancccgacc gctgngcctt atccggaaac tatcntattg agttcaccgc 540
 gnaagacacc acttattntc ctgcagnagn cactggtnac atgattatna nancgaggtg 600
 tttngcngg tctncaagnn ttenttgaan ttt 633

<210> 319
 <211> 645
 <212> DNA
 <213> Mus musculus

<400> 319
 tcttcagcat cttttacttt caccagcgtt tctgggtggg atccaaagcc tccaattatt 60
 attggtatta ctatgaagaa aattataaca aaagcatggg cagttacgat aacattgtaa 120
 atttggatcat ctccataaag tgcacctggt tgacctaat ctgctcgaat taaaatactt 180
 agtgcagtac ccactattcc cgcgggcccg aattcaagct tactcttcct ttttcaattc 240
 agaagaactc gtcaagaagg cgatagaagg cgatgcgctg cgaatcggga gcggcgatac 300
 cgtaaaagcac gaggaagcgg tcagcccatt cgccgccaaag ctcttcagca atatcacggg 360
 tagccaacgc tatgtcctga tagcgggtccg ccacacccag ccggccacag tcgatgaatc 420
 cagaaaagcg gccattttcc accatgatat tcggcaagca ggcacgcga tgggtcacga 480
 cgagatcctc gccgtcgggc atgcgcgcct tgagcctggc gaacagttcg gctggcgcca 540
 gccctgatg ctcttcgtcc agatcatcct gatcgacaag accggcttcc atccgagtag 600
 gtgctcgtc gatgcgatgt ttcgcttggg ggtcgaatgg gcagg 645

<210> 320
 <211> 289
 <212> DNA
 <213> Mus musculus

<400> 320
 gaattcgcgg ccgcgtcgac gccaaagactt cacacagttc tgattgtccc agaagccttg 60
 cgtttgtcaa aacatgacaa tgagatatga aaacttccag aacttggagc gggaagagaa 120
 aaaccaggag atgagaaatg gtgacaagaa aggaggaatg gagtctccaa agtttgcctc 180
 aattccttcc cagtccttcc tgtggcgcat cctctcttgg acccacctcc tctgtttctc 240
 cctgggcctc agcctcctgc tactggtggt catctccgtg attggatcc 289

<210> 321
 <211> 684
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (124)..(153)
 <223> N = A, C, G OR T/U

<400> 321
 acctcagtga tgtgcaaggg tgatcaatga tcggtgagtc tctctcatct cagtgtgtgg 60
 agtgcaagag tagagaactc agatgccaac taattcttga gcatggataa ccaaatttca 120
 gggaggagc cgttttcaat agctaaaagt gcntgagtta taatcacctt gtcacgtttt 180
 gggtgggttc tgaatttgca taccaaccag agcatgaaca ccagtccaca gcatatggca 240
 gcaccaaaca aaatcactcc caccatttcc ttaaagtaag aaaaagcaga ggtaagccaa 300
 gaggtaaagt ctccgagggt cactggttcc actctggtcc cattaaggct caggatctgc 360
 atctgcagtc tcgtctgcaa cttttccagc tcttgcgacc agttccctt caggtaactc 420
 gataggtctg tacttttaat aaaagaatta ttaatatacc tattgggagt aatgcacaca 480
 tgcaaagtgg atgccacaca actcatttgt atgacatcca tcatctgttc catgtcatgt 540
 tgtaaaatat ccactctgat tcactaacat taaccctgag gtgatatgag aatccacct 600
 ttgcagggtg agcaatgcct cagacgtttt ttctgctatc tgacttatag tgtcagcagt 660
 attaatttga tctgccctgg atcc 684

<210> 322
 <211> 719
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (628)..(666)
 <223> N = A, C, G OR T/U

<400> 322
 cttcagcatc ttttctttca ccagcgtttc tgggtgggat ccaggggtgg ggtggaaaac 60
 ttgctaaaaa caaagcaaat gtctttcaat attcacaacc ttaaaattat atccaagaaa 120
 acaaaggata aataattttt tataaaaaata attacttctc aaataacggt tcacaataga 180
 cctgctcaat acatcgatct gactcatctc atctgtgccg cttttcttct ttttaaaatt 240
 ctggcctggg acaaaactac atgaaagaaa gtaccattaa attaagggtt actttccaaa 300


```

aaacaataga aaaatcttaa aagtaaattc acttatatat aaaatattaa ggccctctgca 360
tgagaacggt ttaacatctg ggggaactggc ctttcctaac tgacctatga cccactcac 420
ctcaaacttc agaatgaaag gttctggagt gaaaagtcct tttaattttg ccaatacatg 480
aaattacaca taaaattaca ctgcaaagta atatgtactt aacaaatgat atattgaaaa 540
gtctaacttt ctgctggcta atttcagtat ggacttcaga tcaagtatag tgtattttca 600
gccatatctc ataacttttt gcgacgcngn cgcgaattca agcttactct tncctttttca 660
attcanaaga actcgtcaag aaggcgatag aaggcgatgc gctgcgaatc gggagccgg 719

```

<210> 323

<211> 655

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (16)..(85)

<223> N = A, C, G OR T/U

<400> 323

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gtttagatc tgaaancaag aaagaaggcg gggcttgagg tcctgaggtc acttaagggc 60
cacctnttt gacntaagac ctcantaggc cccgcctcta aaggtttctg acctcaatag 120
gccttcctgg agaactagtt tctaactctc aggcccttgg gacattgcat ctcaagtagta 180
ggtagctctc tacctgtgtt tggcttgctc atgattggca gacactctgc ctggctctgc 240
acagcagcgg ctcagcatca gcatccagct gcttgctgtg tgtagttgt ctacagctg 300
agggctctgc ctgggtact tcaggctttc cggtaggaa gataatttgg tcaattgtgt 360
ctgtggccac tottagaatt ttctcttttg agggaaacctg tgactggttg gcttttgcac 420
tctatggagg gagatggggg taaagactgt ggcaacacac acctccaga agagctggga 480
ccagagactg tcagcacaga aaggacaatg tcttttttag tagctgtggc agacttgagt 540
tgctgtaatt tatacaaatt gtttagaatg gtttttaaga ctaagaaggg aaatatactt 600
attgcacaag actttttataa ttactatact taaattatgc tctatgtggg gatcc 655

```

<210> 324

<211> 677

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (1)

<223> N = A, C, G OR T/U

<400> 324

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necgttagt ttcattttct actttgaggg cacagatgaa aatgtatatc gcaacacagt 60
ggatatcagc ccaagcacga agaccatgct gaacatgcac ccgtacagag tgtacttaaa 120
ggagtcgtca taagggcact gggagccatt ggagcttacc attgtcaggc agtgcagctt 180
acaggaggcc ttttgtccgc agcgcttgat cgatcgccct tgctattcag atgtggtcac 240
agcagcagcc agtttatttg caaagtatgt gtttcttttc ctgttcttac aaatactttc 300
ttctcttaac tcttcaaagg aaacatgaaa tgtgttccgt aaaagtttct agtagattat 360
tcaggaaaat agtctgattt tctggtcgag aaaatccatg agtctggagt ttagttaact 420
gacagaaaat gcagtcaagg aagccaaccc ataaagctga aagtgttaagg aaaaactgtt 480
ccaagtcgga ccagaccagt ccgcgtggaa acttgtgctt cagccgccag ggtccaaacc 540
agctttactt cagtcacaaa cactcgccgt gcgtccgtcc gcccgctcgc ctgggtact 600
tcttccttct ttttatttct aaactttgta tttctacatt gattccggac ggcgataggc 660

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agtcgttttaa gggatcc

677